

FIG. 1

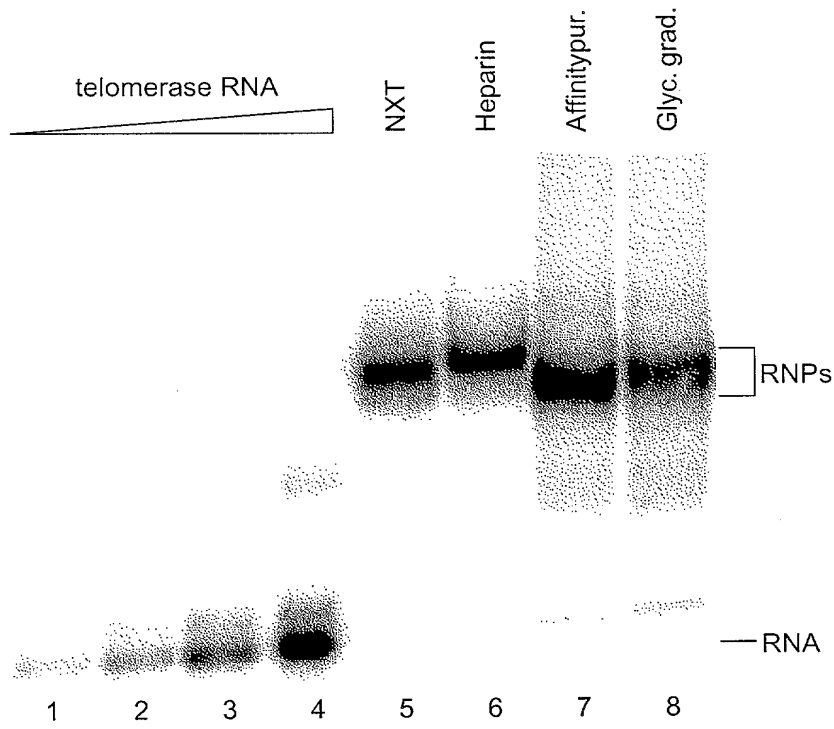


FIG. 2

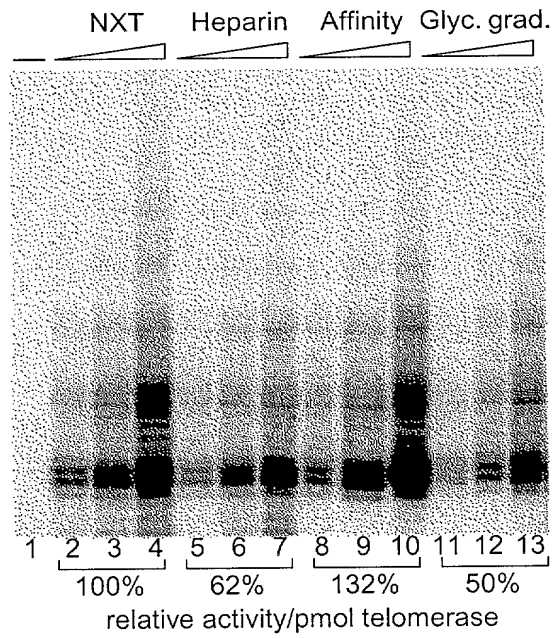


FIG. 3

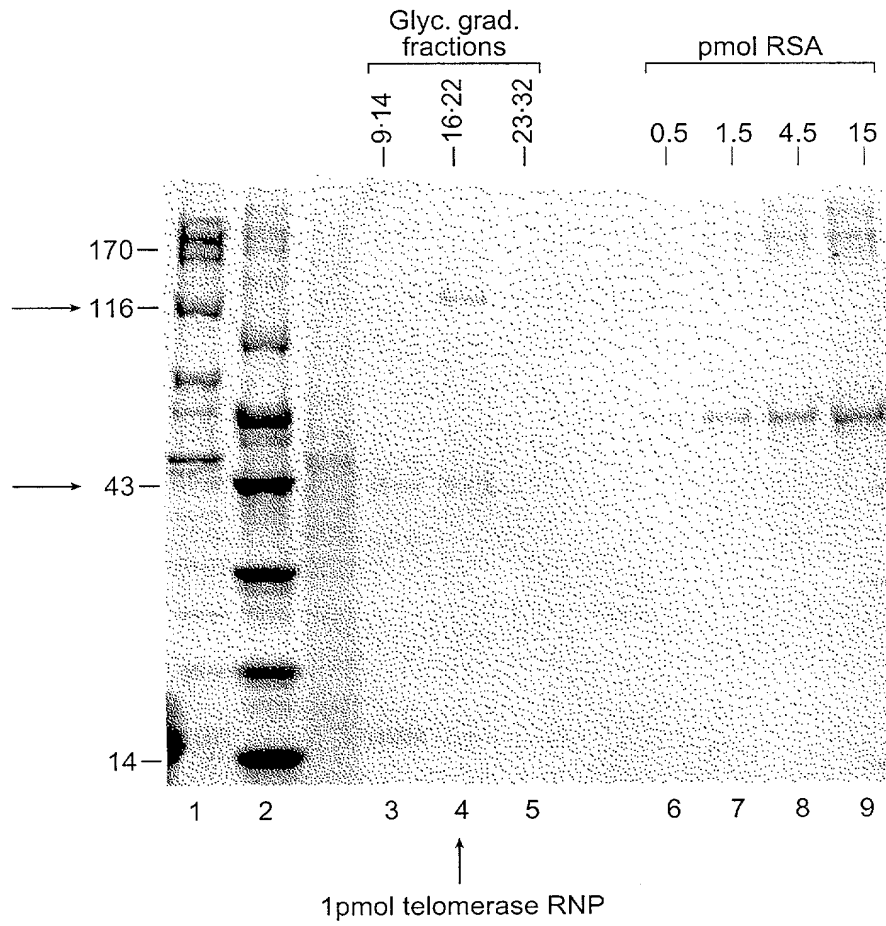


FIG. 4

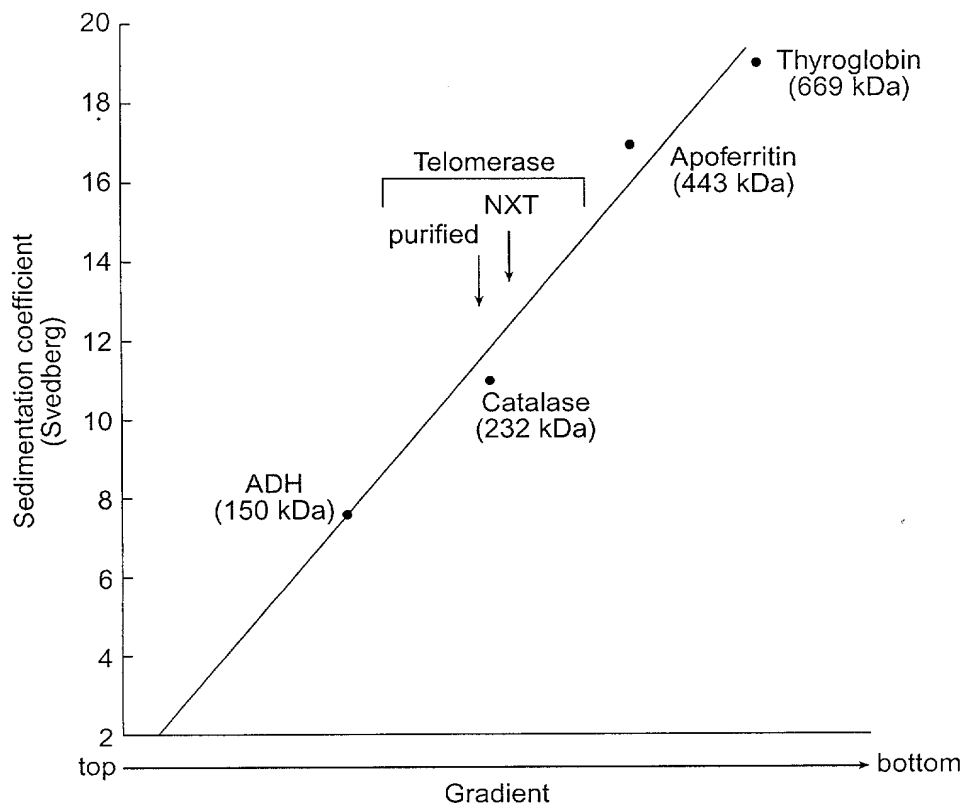


FIG. 5

Telomerase:

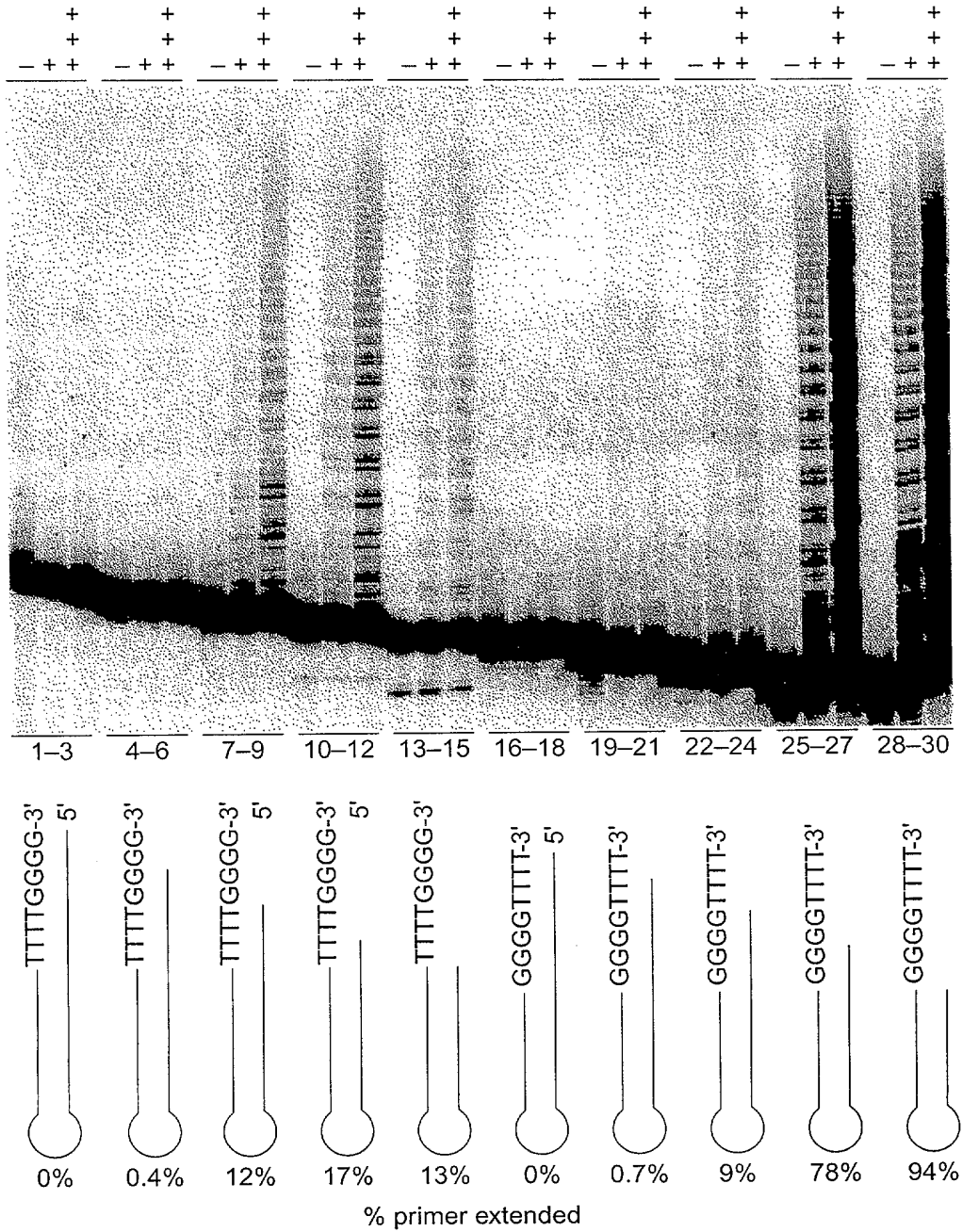


FIG. 6

FIG. 7

FIG. 11

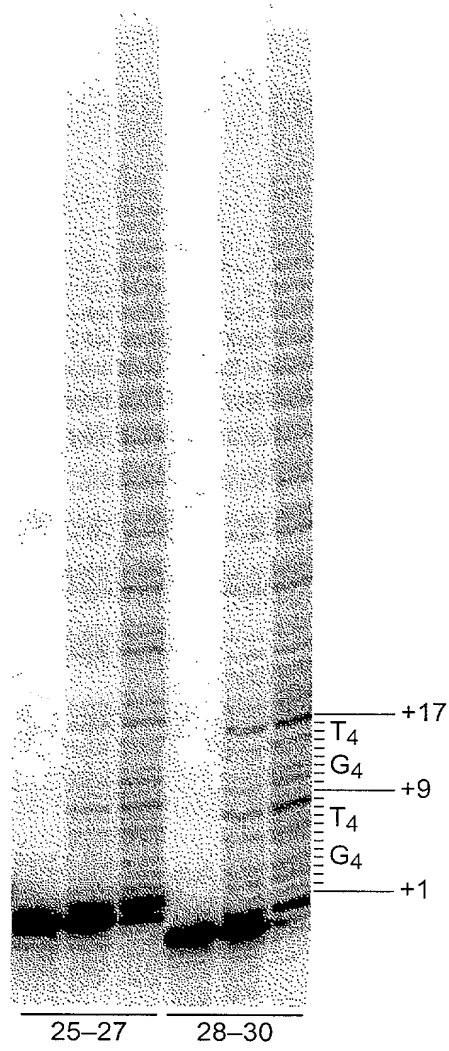


FIG. 8

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1   AAAACCCCAA AACCCCAAAA CCCCTTTT TAG AGCCCTGCAG TTGGAAATAT
51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCa
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCaA
501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAACTTCT GAAGGAACCTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACCTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC
1301 AAAAECTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAC CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAAAGAAA AAGTATGAGG
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAACCT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAECTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTT TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACCTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

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FIG. 9

2401	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTTAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACCTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTCCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTCTAAC	TTATTTTGGG	AAGTTAATTT	TCAATTTTGT	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG		

FIG. 9
(CONTINUED)

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWQKQVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFQRTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGGGA
201	ADMNEPRCCS	TCKYNVKNEK	DHFLNNINVP	NWNNMKSRT	IFYCTHFNRN
251	NQFFFKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAYM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYEEELFS
351	YTTDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHელი
401	KNLLEKINT	REISWMQVET	SAKHFFYFDH	ENIYVLWKL	RWIFEDLVVS
451	LIRCFYVTE	QQKSYSKTY	YRKNIWDVIM	KMSIADLKKE	TLAEVQEKEV
501	BEWKSLGFA	PGKLRLIPKK	TTFRPIMTFN	KKIVNSDRKT	TKLTTNTKLL
551	NSHMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDYF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKKDNLL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFYY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLNMQT	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTITTE	DFANKTLNKL	FISGGYKYM	Q	CAKEYKDHFK
951	LEVSKIYYSV	TRAFFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNRVCM	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 10

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CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTGAGGTAGTTTAGA
1  -----+-----+-----+-----+-----+-----+-----+ 60
GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTCTTTTTTAACCTCATCAAATCT

a P Q N P K T P K P L * K K K K L R * F R -
b P K T P K P Q N P Y K K R K N * G S L E -
c P K P Q N P K T P I K K E K I E V V * K -

AATAAAATATTATTTCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
61 -----+-----+-----+-----+-----+-----+ 120
TTATTTTATAATAAGGGCGTGTTCACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a N K I L F P H K W R W I L I W M I * K I -
b I K Y Y S R T N G D G Y * F G * Y R K F -
c * N I I P A Q M E M D I D L D D I E N L -

TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
121 -----+-----+-----+-----+-----+-----+ 180
ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a Y F L I H S T S I A A L V V T R K D A K -
b T S * Y I Q Q V * Q L L * * Q E R M Q N -
c L P N T F N K Y S S S C S D K K G C K T -

CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAAACAATTAG
181 -----+-----+-----+-----+-----+-----+ 240
GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a H * N L A R N R L H * L F Q S C K N N * -
b I E I W L E I A F I D Y S K V A K T I R -
c L K S G S K S P S L T I P K L Q K Q L E -

AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAAATTAGTTTTAA
241 -----+-----+-----+-----+-----+-----+ 300
TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAATTT

a S S T S R M Q I F I T I L S * E N * F * -
b V L L L G C K S L * R F F L E K I S F K -
c F Y F S D A N L Y N D S F L R K L V L K -

AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
301 -----+-----+-----+-----+-----+-----+ 360
TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a K A E S K E * K L K H Y * C L N K I R * -
b K R R A K S R N * N I T N V * I K S G N -
c S G E Q R V E I E T L L M F K * N Q V M -

TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
361 -----+-----+-----+-----+-----+-----+ 420
ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a * G L F Y F L D H F L R S I M E K I T * -
b E D Y S I F * I T S * G A L W R K L L N -
c R I I L F F R S L L K E H Y G E N Y L I -

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FIG. 12

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TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTAA

a Y * K V N S L D Y F P S Q Q * * V Y * I -
b T K R * T V W I I S L A N N D E Y I K F -
c L K G K Q F G L F P * P T M M S I L N S -

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
GTATACTCTTACTCAGTTTCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H M R M S Q R I S I H Q T Y Q R Q T R Y -
b I * E * V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L * -

AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTTCG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
TTTTGCGTTCTTTTTCAAACCTATTAGCTTGTCTGTTCTTGAATAACGTAAATGATAAGC

a K T Q E K V * * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -

TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTGA

a Y G F Y Y N C F R Y R R * T P E S * D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -

TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
ACTTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a * K S C L Q L K E S Q F * K F * C V C H -
b E K A V Y N * R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -

TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L * I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -

CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T M Q V * W N I R * I L W D K C T L -

TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
ACTTAAATATAACCTAAGAATTTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a * I Y I G F L K H R Y T E C F R D * F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y W I L K A * I H R M L * R L I * L -

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FIG. 12
(CONTINUED)

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          TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
901  -----+-----+-----+-----+-----+-----+-----+-----+ 960
          AATGTTGTCTAATGGACAAAATAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a  L Q Q I T C F D Y S C S S L I S L K E A -
b  Y N R L P V L I T L A H L L Y L * K K Q -
c   T T D Y L F * L L L L I S Y I F K R S R -

          GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAATTTGTTGATTCTTCTGTAACC
961  -----+-----+-----+-----+-----+-----+-----+-----+ 1020
          CCGCTTACTTTTCTTCTGATTCTTTCTCTAAAGTTTAAACAATAAGAAGACATTGG

a  G E M K R R L K K E I S K F V D S S V T -
b  A K * K E D * R K R F Q N L L I L L * P -
c   R N E K K T K E R D F K I C * F F C N R -

          GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTCT
1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
          CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTTCTTCTCTCGATAGTGTTAGGACTAAG

a  G I N N K N I S N E K E E E L S Q S * F -
b  E L T T R I L A T K K K K S Y H N P D S -
c   N * Q Q E Y * Q R K R R R A I T I L I L -

          TTAAAGATTTCAAAAATTCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
          AATTTCTAAAGTTTTTAAAGGTCCATTCTCTCTATGTAAGTAATTTTAAAGTATATAATATC

a  L K I S K I P G K R D T F I K I H I L * -
b  * R F Q K F Q V R E I H S L K F I Y Y S -
c   K D F K N S R * E R Y I H * N S Y I I V -

          TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTGATTAGCTGGAA
1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
          AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

a  F F I S Q L L F S F I L T I F F D * L E -
b  F S F H S C Y F L L S * Q Y F L I S W K -
c   F H F T A V I F F Y L N N I F * L A G S -

          GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAAGTCTTATTCACATTCAT
1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
          CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a  V K S I K * E K R * T E V T * L I H I H -
b  * K V S N K R S A R L R * L S L F T F I -
c   K K Y Q I R E A L D * G N L A Y S H S * -

          AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
          TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTT

a  R S T F I Y P I R * * G N S S H P F * K -
b  D R P S Y I Q Y D D K E T A V I R F K N -
c   I D L H I S N T M I R K Q Q S S V L K I -

          TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
          ATCAGGATACTCCTGATTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a  * C Y E D * I F R V K K W S R N L N Q K -
b  S A M R T K F L E S R N G A E I L I K K -
c   V L * G L N F * S Q E M E P K S * S K R -

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FIG. 12
(CONTINUED)

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GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
 1381 -----+-----+-----+-----+-----+-----+-----+ 1440
 CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L * I F R * * V L P -
 b N C V D I A K E S N S K S F V N K Y Y Q -
 c I A S I L Q K N R T L N L S L I S I T N -

ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
 1441 -----+-----+-----+-----+-----+-----+-----+ 1500
 TAGAACTAACTAATTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a I L I D C R D * R G N C T E D H * R N K -
 b S * L I E E I D E A T A Q K I I K E I K -
 c L D * L K R L T R Q L H R R S L K K * S -

GTAACCTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
 1501 -----+-----+-----+-----+-----+-----+-----+ 1560
 CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
 b * L L L I R E * T K L L I * R S A I F N -
 c N F Y * L E N K L N Y * Y R D Q R S S I -

TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
 1561 -----+-----+-----+-----+-----+-----+-----+ 1620
 AACTGCTTTTATTTTCGACTTGATTTCAATCTGTTATTTTATGTTTGAACCAAGTTT

a L T K * K L N * S * T I K N T N L G Q N -
 b * R N K S * T K V R Q * K I Q T L V K I -
 c D E I K A E L K L D N K K Y K P W S K Y -

ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAATAAAATGA
 1621 -----+-----+-----+-----+-----+-----+-----+ 1680
 TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTATTCCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q * I K * -
 b L R K E K K T S * Q K K K * G N K * N E -
 c * G R K R R P V S K R K N K A I N K M S -

GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
 1681 -----+-----+-----+-----+-----+-----+-----+ 1740
 CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAGTTATTAATAAATTTTCTCCCCAA

a V Q K * R N K R F I F F N N L L K R G V -
 b Y R S E E I K D L F F S I I Y * K E G F -
 c T E V K K * K I Y F F Q * F I E K R G F -

TTGGGGTTTTTGGGGTTTTTGGGG
 1741 -----+-----+-----+-----+-----+-----+-----+ 1762
 AACCCCAAAACCCCAAAACCC

a L G F W G F G -
 b W G F G V L G -
 c G V L G F W -

FIG. 12
 (CONTINUED)

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798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
PGDEL RPSMQKLLQEKGLGG..TDFPYECIDEWTKNKTHVD 617
 847 WIGISIDMKTLALMPNINLRIEGILCTLNLMQTKKASMWLKKKLKSFLM 896
KVKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGGYKMQCAKEYKD.HFKKNLAM 945
KCLNLGDEFNENNYIKIFGM 687
 654 PNIKIF...AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYDPDFLSTLKHFI 995
NMVE 706
 688 SDSI.....LKFISAKQGA.....NMVE 706
 996 IFSTKKYIFNRVC 1008

 707 VI..KNFALQKIG 717

FIG. 13
(CONTINUED)

132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
 1 MSRRNQ.....KKPQAPIGNETNLDVFLQNLEVYKSQIEHYKTQQQQI 43
 179 GNNVFDHLKVNDKFDKQKGAADMNEPRCCSTCKYNVKNKEDHFLNNIN 228
 44 KEEDLKLKFKNQDQDGNNGDDDEE.....NNSNKQQLRRVN 84
 229 VPWNWNMKSRTIRIFYCTHFNRRNQFFKKHEFVSNNKNNISAMDRAQTIFTN 278
 85QIKQVQLIKK...VGSKEKDLNLDENKKN 114
 279 IFRFNRIKKLKDVKIEKIAYMLEKVDFNFNYLTSCPLPENWRERKQ 328
 115 GLSEQQVKEEQRLTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164
 329 KIENLINKTREEKSKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFEISHDQK.....NYVSIYANQKTSYCWWLKDYFNK 200
 378 RNRKNFQKKVKYVELNKHLEIHNLLLEKINTREISWMQVETSAKHFFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLRLWI..FEDLVVSLIRCFYVTEQQKSYSKTYYYRKN 475
 243 VNFDDNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKMSIADLKKETLAEVQKEVEEWKSLGFAPGKLRLIPKKTFRP 525
 291 FAVVFSHR.....HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330
 526 IMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKNRMFKDPFGFAVFNY 575
 331 VYSFSTDLKLDV..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378

FIG. 14

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576 DDVMKKYEEFVCKWKQVGQPKLF.FATMDIEKCYDS..VNREK 615
 : : : | | : : : | | : : : | | : : : | : : : | : : : |
 379 NVLLKKVKH ANLNLVSIPTQFNDFYFVNLQHLKLEFGLEPNILTKQK 426
 516 LSTFL.....KTTKLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK 657
 | : : | | : : | | : : | | : : | | : : | | : : | : : : |
 427 LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ 476
 558 DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKT LIVEAKQRNYFK 705
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 477 EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN....LQATQEIY.. 520
 706 KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYATLEE 755
 | : : | | : : | | : : | | : : | | : : | | : : | : : : |
 521 .DSLHKLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.....YETLNN 564
 756 SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVL FIEKLINVS 305
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 565LKRCSVNISNPHGNISYELTN.....KDSTFYKFKLT LNQE 500
 806 ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855
 | : : | | : : | | : : | | : : | | : : | | : : | : : : |
 601 LQHAKYTFK..QNEFQFN NVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
 856 TLALMPNINLRIEGILCTLNLNMQT..KKASMWLKK..KLKSFLMNNITH 901
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 649 NVNI.....IASLLYPNNIQKNPFPKNP NLLFFKQFEQLKNLE NVSINC 691
 902 YFRKTI...TTEDFANKTLNKLFI SGGYKYMQCAKEYKDHFKKNLAMSSM 948
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 692 ILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKL FKT LQQLPEL 741
 949 IDLEVSKIIYSVT.....RAFFKYLVCNIKDT..IFGEEHY 982
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 742 NQVYINQQLBELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF 791
 983 PDFFLS TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKS DQCQSLIQ 1028
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 792 DQNTVSDDSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQELLK 840

FIG. 14
(CONTINUED)

4 DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK..... 47
 : : : | | : : : | | : : : | | : : : | | : : : | : : : |
 617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP 666
 48LQKQLEFYFSDANLYNDSFLRKLVLKS GEQRVE....IETLLM 86
 : : : | | : : | | : : | | : : | | : : | | : : | : : : |
 667 FNKPNLLFFKQFEQLKNLE NVSINCILDQHILNSISEFLEKNKKIKAFIL 716

FIG. 15

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1 MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS... 42
  |:|. . . .| | . . .| . . .| | . . .| | . . .| | . . .
491 IELAIIAVNKNLDEIKGHTAIFSDVSGSMSTSMSSGAKKYGSVRTCLEC 540

43 .LTIPKLQKQ.....LEFYFSDANLYNDSFLRKLVLKSQEQRVEIETLL 85
  |:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNCYL.EVDLPGDELPRSMQKLL 589

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FIG. 16

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telomerase p43 LQKQLEFYFSDANLYNDSFLRKLVLKSQEQRVEIETLLM
human La ICHQUEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA ICEQIEYYFGDHNLPDKFLKQOI.LLDDGWVPLETMIK
Drosophila La ILROVEYYFGDANLNROKFLREQIGKNEDGWVPLSVLVT
S. c. Lhplp CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT

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FIG. 18

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1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
61 tagatttaatt ttagaaaagta tcaattgaaa aatggaaaatt gaaaaacaact aagcacaata
121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
181 tatataagtt aggggttaaga ttgacgatcc taagcaatat ctctgtaacg tcaactgcagc
241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
301 taaagcactt cttgaggttg ctgagctcga tcttgagttc atctgctagt tggcagttca
361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
541 caaaaatttg tatcttgata ggatacttcc ataagatatt cgttaaggaac tcactttccg
601 taagtgttta caaagatgag tcagaagcaa gttttctgaa ttcaacgaat actaactttg
661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttaacctc ttttgcctaa
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
841 agatgcaatc aaggctttta aaccagcagt tatgaagaaa atagccaaga gatagaatgc
901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggaaat caaagactct
961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca ccttcaatc ctgaattggc tggaaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcataagg caacactgct gaggtttggg ataatttaatt
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cgggtgttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gaggtaactca atgtcagggt gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gaggtcattg atgaatggac
1921 aaagaataaaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagttaaat cctaactata aaatccttgc agttgactta gaaggttacg gaaagtgcc
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcacccac tttttgtttt tattgcatga ccattatgaa atttaaatat ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagttctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a

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FIG. 19

	Motif A	Motif B
Consensus	h--hDh---h--h	h---+-QG---sp
telomerase p123	GQKLFATMDIEKCYDSVNREKLSFLKTKLL-100-KFYKQTKGIPQGLCVSSILSSFYATLEESSLGFL	
Dong (LINE)	KNRNLHCTYDDYKKAFFDSIPHSWLIQVLEIYKIN-28-RQIAIKKGIYQGDLSPLWFCIALNPLSHQLHNR	
al S.c. (group II)	FGSNWFREVDLKKCFDTISHDLIIKELKRYISD-26-HVPVGPVRCVQGAFTSPALCNVLLRLDRRLAGLA	
HIV-RT	LKKKKSVTVLVDGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLPQGWKGSIPAIFQSSMTKILEPFRKQN	
L8543.12	VLPELYFMKFDVKSCYDSIPRMECMRIILKDALKN-68-KCYIREDEGLFQGSLSAPIVDLVYDDLLEFYSEFK	
	Motif C	Motif D
Consensus	h--YhDdhhh	Gh-h---k
telomerase p123	-14-LMRLTDDYLLITQENN-0-AVLFIKLIINVSRENGFKFMKKLQT-23-QDYCDWIGISI	h-hLgh-h
Dong (LINE)	-16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ	
al S.c. (group II)	-55-YVRYADDILIGVLGSKN-2-KIIKRIIDNNFLNS.LGLTINEEKTLLI-4-ETPARFLGYNI	
HIV-RT	-4-IYQYMDLLYVGSHEIG-1-HRTKIEELRQHLRLRWGLTTPDKKHQK-0-EPPFLWMGYEL	
L8543.12	-8-ILKLADDFLIISTDQQQ.....VINIKKIAMGGFQKYNKANR-41-IRSKSSKGIFR	

FIG. 17

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MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
 VNVTAACLLQEGSYQQDKDERRYITKALLEVAESDPEFICQLA
 VYIRNELYIRTTTNYIVAFVCVHKNTQPFIEKYFNKAVLLPNDL
 LEVCEFAQVLYIFDATEFNLYLDRILSQDIRKELTFRKCLQRC
 VRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTKKK
 RKENLLTKLQAIKESSEKSKRETGDIMNVEDAIKALKPAVMKKI
 AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
 YKILGKKYPKTEEBYKAAFQDSASAPFNPPELAGKRMKIEISKW
 ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
 HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
 ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
 KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMGGA
 KKYGSVRTCLECALVGLVMVKQRCEKSSFYIFSSPSSQCNKCYL
 EVDLPGBELRPSMQKLLQEKGLGGTDFPYECIDEWTKNKTHV
 DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
 VDLEGYKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
 VEVIKNFALQKIGQK

FIG. 20

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK
 EEDLKLKFKNQDQDGNNGNDDDDDEENNSNKQELLRRVNQIKQ
 QVQLIKKVGSKVEKDLNLDENKKNGLSEQQVKEQLRTITEE
 QVKYQNLVFNMDYQLDLNESGGHRRHRETQDYDEKWFIEISHDQ
 KNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAEFY
 AFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLSLERF
 NILNIRSSYTRNQYNFEKIGELLETFIVVFSHRHLQGIHLQVP
 CEAFQYLVNSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
 LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSI
 TQFNDFDYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNL
 KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
 ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLII
 RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCVNI
 SNPHGNISYELTNKDDSTFYKFKLTNLQELQHAKEYTFKQNEFQFN
 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
 NIQKNPFPKNPLFFKQFQELKNLENVINCILDQHILNSISEF
 LEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPELNQVYINQ
 QLEELTVSEVHKQVWENHKQKAFYEPLCEFTIKESSQTLQLIDFD
 QNTVSDDSIKKILESISESKYHHYLRNPSQSSSLIKSENEEIQ
 ELLKACDEKGVLVKAYYKFPLCLPTGTYDYNSDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKGHFNGLDEILTTCFAL
 PNSRKIALPCLPGDLSHKAVIDHCIYLLTGELYNNVLTFGYKI
 ARNEDVNNSLFCHSANVNVTLKGAAWKMFHSLVGTIYAFVDLLI
 NYTVIQFNGQFFTQIVGNRCNEPHLPKQVQRSSSSSATAAQIK
 QLTEPVTNKQFLHKLINSSSFFPYSKILPSSSSIKKLTDLREA
 IFPTNLVKIPQRLKVRINLTQKLLKRHKRLNYVSIILNSICPPL
 EGTVDLDSLHLSRQSPKERVLFIIIVILQKLLPQEMFGSKKNKGK
 IIKNLNLLLSLPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH
 NFENLNQLAICFISWLFRLIPKIIQTFFYCTEISSTVTIVYFR
 HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMKRI
 IPKKSNNEFRIIAIPCRGADEEEFTIYKENHNKNAIQPTQKILEY
 LRNKRPTSFTKIYSPTQIADRIKEFKQRLKKFNNVLPPELYFMK
 FDVKSCYDIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
 KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIEFKTA
 LWVEDKCYIREDGLFQSSLSAPIVDLVYDDLLEFYSEFKASPS
 QDTLILKLADDPLIISTDQQQVINIKKLAMGGFQKYNANANRDK
 ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMMNFHRSKS
 SKGIFRSLIALFNTRISYKTIDTNLSTNTVLMQIDHVKNISE
 CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
 YEVRFITLNGFLESLSNTSKFDNIIILRKEIQHLQAYIYIYI
 HIVN

FIG. 23

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1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaaat cttgattttg tattacaaaa
121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
301 gattaagtag caagtttaat tgataaaaaa agttgggtct aaggtagaga aagatttgaa
361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
421 attagaacg attactgaag aatagggttaa gtattaaaat ttagtattta acatggacta
481 ccagtttagat ttaaatgaga gtgggtggcca tagaagacac agaagagaaa cagattatga
541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
601 ctaaaagaca tcatattggt ggtggcttaa agattatttt aataaaaaaca attatgatca
661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgctt ttgatgattt
721 ttcacaaaaca atcaaaactta tcgcattgct tagattttta ttatcactag aaagattcaa
781 tgataataat ctctgtatac cttatacaag aaattaatat aatttttgaga aaattgggtg
841 tatttttgaa ataagatctt cagttgtctt ttctcatcgc cacttacaag gcattcattt
901 gctacttgaa actatcttcg tgcgaagcgt tctaataatt agttaactcc tcatcataaa ttagcggttaa
961 acaagttcct ttatagggtat actctttctc tacagactta aaattagttg acactaacia
1021 agatagctaa ttttttaagt tcttataaga attcctcgt ttgactcatg taagctagta
1081 agtccaagat gttagtgtta ctaacgctgt agagaacctc aatgttttac ttaaaaagggt
1141 ggctatccca aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1201 caagcatgct taacatttga aattagagtt tggattagaa ccaaatatth tgacaaaaca
1261 tgtttaattta aatctacttt tgagtataaa ataatacaaaa aatcttaaat ttttaagatt
1321 aaagctttac acctacgttg cttagaagaa ctcagaaaaa cagatattaa aacaagctac
1381 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1441 aactccaagc gaaagcacia gtggtatgaa attttttgat catctttctg aattaaccga
1501 ccttggaagat ttcagcggtta acttgtaagc tacciaagaa atttatgata gcttgcaaa
1561 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaatgga
1621 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1681 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1741 taaagattct actttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1801 gtatactttt aagtagaacg aatttttaatt taataacggt aaaagtgcaa aaattgaatc
1861 ttcctcattt gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1921 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
1981 tcccttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2041 aaatgtatct atcaactgta ttcttgatca gcatataact aattctattt cagaattctt
2101 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2161 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2221 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2281 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaacc
2341 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2401 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2461 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2521 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2581 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaatat
2641 tgaatattht tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2701 atatattht gttatttaatt tcattattht aagtaataaa ttatttttca atcatttttt
2761 aaaaaatcg
2821

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FIG. 21

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Oxytricha
EuplotesLCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 24

ATTTATACTCATGAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
 GACCAACAGTACTTACAAAGAAAATTTAAATGTGGTCACTTCAATGGCCCTCGATGAAAT
 TCTAACTACGTGTTTTGCACTACCAAATTCAGAAAAATAGCATTACCATGCCCTTCCTGG
 TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
 ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
 TCTTTTTTGCCATTCTGCAAATGTAAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAAT
 GTTCCACAGTTTGGTTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
 GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
 ACTTACAGAACCAGTGACAAATAAAACAATTCCTTACACAAGCTCAATATAAAATTCCTCTTC
 TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
 GAGAGAAGCTATTTTTCCACAAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
 TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
 GAATAGTATTTGCCACCATTTGGAAGGGACCGTATTGGACTTGTGCGATTTGAGTAGGCA
 ATCACCAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAAGTTATTACCCCA
 AGAAATGTTTGGCTCAAAGAAAAATAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
 AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAAA
 GGATTTTCGGTGGTTGTTTCATTTCTGATATTTGGTTTACCAAGCACAAATTTGAAAACCT
 GAATCAATTGGCGATTTGTTTCATTTCCCTGGCTATTTAGACAACTAATTCCTCAAAATTTAT
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTTGTTTACTTTAGACA
 TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAAGACGTACTTAGT
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTTCAAGATTATTGCCATCCCATGCGAG
 AGGGGCGAGACGAAGAAGAAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
 CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTACTAAAATATA
 TTCTCCAACGCAAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAAT
 TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAATGAAAATGGGTT
 TTTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAATATTTAAAACAGCTTT
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
 TGCTCCGATCGTTGATTGTTGTTGATGACGATCTTCTGGAGTTTATAGCGAGTTTAAAGC
 CAGTCCTAGCCAGGACACATTAATTTTAAACTGGCTGACGATTTCTTTATAATATCAAC
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
 TGCGAAAGCCAATAGAGACAAAATTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
 TATTTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAACATTCAAG
 CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAAT
 AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCACAAA
 CACCGTTCTCATGCAAAATGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
 TTTTAAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCATTCGTTCTTACAACG
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
 TGAGGTACGATTACCATATTTGAATGGATTTTTTGAAAGCCTATCTTCAAACACATCAAA
 ATTTAAAGATAATATCATTTCTTTTGAGAAAGGAAATTCACACTTGCAAGC

FIG. 26

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[illegible]

FIG. 25

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AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 27

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGAGACCACGTTTCAAAGAACAGGCTCTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTGGAAGCAGAGGTGAGGCAGCATCGGGAAGC
CAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNK SARKEVSWNSISISRF SIF YRSSYKFKQDLYFNLHSICDRNTVHMLWQWIFPRQFG
LINAFOVKQLHKV IPLVSQSTVVPKRL LKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIF EII LKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKR SNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESDLRNRTVYFRKDIWKLLCR
PFITSMKMEAF EKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN
QTLRPVASILKHLIN EESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKKLDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVQLLSMKTSDTL FVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVD DFLFITVNKKDAKFLNL SLRGFEKHN FSTSLEKTVINFENSNGI INNTFFNESKKRMPFFG
FSVNMRLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMDIFIPQRMFITDLNVI GRKIWKKLAEILGYTSRRFLSSAEVKWLFCL
GMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF LHRRIAD

FIG. 29

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ggtagccgatttactttccctttcttcataagctaattggttcctcgcgaacgcctcctaaactctctggaaaatatttttacaaga
actcaataaacaataaccaagtcaaatcccaatagaaggtgtatttagtgatcgataaattctattttatcggtcgtta
ccaagtataaggacaaaagaacaacttcctcccccataagaacttttacttttataaattacttttcaaatatatttcg
gggtcgttacttttaactcggtgactgttttagctgctacttctagccaacccggtgtttctaccccgctcatggatat
agctcttgaggtagtcacagaaatccttacaaatccttgatgagactatatagattcattacacgctgcgtgcatattc
ttaacatggagccttacactttagatgagtcacgtcgcatgaggtatttggtatcattccaacgtttgctctgaaaa
gttgataattttgcaaaatcatgcttagtggtgttaacccggaagttttttgatgcttgacacgcttagcatg
attgagataattcaaaaatttctatccactacaactcctttaacggtttttattttctatttctcatgttctggtt
ccaaatattgatcatcctcgattaggcttttccgttttactcctggaatcgtaaccttttccactattccccctaata
ataactaaattagtttcgcttataattgatagtagaagaattggtgatctactcgtgtaattgtatttagtttaa
gatactttgcaaaaacatttatagctatcatatataaaaaaaacccataaattataaattaatcaatatttgcggtc
actattttataaacggttatgatcagtaggacactttgcatatatatagttatcgttaattggttacttgaacttgcat
GACCGAACACCATACCCCCAAAGCAGGATCTTCGCTTCTAGAGATCAATATGTATACCTATGTACTTAATGATT
ATGTACAACTGTTTGGAGGGTCGCGGAAGTCGTATAGCAATATATCGAAACGCTTGAGAAGCGATGACAAACG
TCCTTTCTATTTTCTTCATTCGACTGTAGTCGGCTCGACAGTAAGCAGATGAAGGTGTTCAATTTTCTCCAAA
ATGCTCAGTCAGAGgtatatattttgttttatttttctattcgggatagctaatatagggcagCTAATAGC
GAATGTTGTAACACAGATGTCGATGAAGTTTTGAGCGTCGAAGGAATCTACTGTAGAAAGGTTTTCATGgttaagg
attctaattgtgaaatatttacctgcaattactgtttcaaaagagattgtatttaaccgataaagAATCATGAAGATTTC
GAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTTAATTTACTATATCTAGTGAATCAAAA
AATTGGCAACTTTGTTAGAAATgtaaatccgggttaagatgttgccactttgaaacagactgacaagtatagTATCGG
CAGTGATGCCATGCATTACTTATATCCAAAGGAAGTATTTTGAGGCTCTCCAAATGACAATTACCCTCAGATTTCG
GCATACCACTTTTAAATAATGTGTTGAGGAAACCTGTCTCAAAAAGAAAGCAACCATTGAAACATCCATTACT
CAAAAATAAAGCGCCGCAAGAGTTTCCCTGGAATAGCATTTCAATAGTAGGTTTAGCATTTTTCACAGTCTATCCTA
TAAGAAGTTTAAGCAAGgtaactaactgttatccctcataactaatttagatCTATATTTTAACTTACACTCTATTT
GTGATCGGAACACAGTACATGTGGCTTCAATGGATTTCGAAGGCAATTTGGACTTATAACCGCATTCAGTGAAG
CAATTGCACAAAGTGATTCACATGGTATCACAGAGTACAGTGTGCCAAACGTCCTCAAAGGTATACCTTTAATTGA
ACAAACAGCAAGCGACTCCATCGTATTTCTATCAAAAGTTTACACCATTATTGCCCATATATTGACACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCGCAACCGAGTGTTCGCTTCTTCGATCCATCTTGTTCGAGTGTTCCT
AAATTAATCTGGGGTAAACCAAGGATATTGAGATAATAATAAAGgtattgtataaaatttaccactaacgatttt
accagACCTCGAAACTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTACATTATTAATGAGTAACATAAAGtaa
tatgccaaattttttaccatttaattacaatcagATTTCAGAAATTGAATGGCTAGTCTCTGGAAAAAGGTCAAATGCG
AAAATGTGCTTAAGTATTTTGAGAAACGCAAGCAAAATATTGCGGAATTCATCTACTGGCTATACAATCGTTTATAAT
ACCTATTTTACAATCTTTTATATCACTGAATCAAGTGATTTACGAAATCGAACTGTATTATTAGAAAAAGATATTT
GGAAACTCTGTGCGGACCTTTATTACATCAATGAATAAGGAGCCTTTGAAAAAATAAACGAGgtattttaaagtatt
ttttgcaaaagctaatatttcagACAAATGTTAGGATGGATCTCAGAAAACTACTTTGGCTCCAGCAGTTATTCGT
TATTACCTAAGAAGAAATACCTTTCGTCTCATTTACGAATTAAGAAAAAGATCTTAATAAAGgtattttaaagtatt
caatgactttacttctaactattattagcagATGGGTTCAACCAAAAAAATGTTAGTCAGTACGAAACCAACTTTACG
ACCTGTGGCATCGATACTGAAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTAACTTGGAGGTTTACATGAAGC

FIG. 30

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TTCTTACITTTTAAAGGATCTTCTTAAGCACCGAATGTTTGGGtaattatataataatgcgcgattccctcattataatttt
gcagGCGTAAAGAAATTTGTACGGATAGATATAAATTCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATT
GTTAAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAAGTACCGAGCTACAAA
AAACTTTGTTAGTGAGGCGTTTCTATTTgaagtttatttttcatgggaattttttaaacaattcttttttagTTGAT
ATGGTGCCCTTTTGAAAAAGTCGTGCGTACAGTTCTTCTATGAAACATACAGATACATTTGTTTGTGATTGTTGATTATG
GACCAAAAGTTCTTCTGAAATTTTAAATGCTCAAGGACATCTCTGAGACACATTTGTTAAAGTataaccaattgttga
attgtaataaacactaatgaaactagATAGGAAATTTCTCAATACCTTCAAAAAGTTGGTATCCCTCAGGGCTCAATTTCTGT
CATCTTTTGTGTCATTTCTATATGGAAGATTTGATTCATGAATACCTATCGTTTACGAAAAGAAAGGATCAGTGTG
TTACGAGTAGTCGACGATTTCTCTTTATAACAGTTATAAAGGATGCAAAAATTTTGAATTTATCTTTAAAGAG
tgagttgctgctcattcctaagttcctaaccgttgaagGATTTGAAAAACACAAATTTTCTACGAGCCTGGAGAAAAACAGTA
ATAAACITTTGAAAAATAGTAATGGGATATAAACAATCTTTTATGAAAGCAAGAAAAGATGCCATCTTTCGGTTT
CTCTGTGAACATGAGGTCTCTTGATACATTTGTAGCATGTCCTAAATTTGATGAAGCCTTATTTAACTACATCTGTAG
AGCTGACGAAACATATGGGAAATCTTTTTTTACAAAATTTAAAGTatactgtgaactgaataatagctgacaaata
atcagATCGAGCCTTGCAATCCTTTGCAAGATTTTATGACATTTACCACAATTTCAAAATTTCAATTTCTGCTGCAATAT
ATATAGGCTAGGATCTCTATGTGTATGAGAGCACAGCATACTTAAAGGATGAAGATATATTTATTTCCCAAGAA
TGTTTCAACGCGgtgagtaacttattttaaactagaaaagtcattaatccttagATCTTTTGAATGTTATTTGGAAGAA
AATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGATGAGCGTTTCTTGCTCTGAGAGTCAAAATGgtacgtgt
cggctcgcgagacttcagcaatattgacacatcagGCTTTTGTCTTTGGAATGAGAGATGGTTTGAAACCTCTTTCAA
TATCATCCATGCTTCGAACAGCTAATATACCAATTTCAATTTCACTGATCTTATCAAGCCGCTAAGACCAAGTTTGGC
ACAGGTGTTATTTTACATAGAAGATAGCTGATTAATgctcattttcaatttattataacatcctttattactggtgtc
ttaaacaattattactaagtatagtgaccccccaagcaagcatactataggattcttagtaaaagtaaaataatctc
gtattagtttttgattgacttgctttatccttatactttaaagaaagattgacagtggttgctgactactgccccacatg
ccccattaaacgggagtggttaaacattaaaaagtaatacatgaggtcattcctttcatttagaataaggaaagtggttt
tctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttaaacaaaggggatttaagcatatccgaagg
aaaagagagtaataatacccagtggtgtgaagaaagcaaggataatttggaacaagcttcgacagtgacaggctaaatt
ttggtagccgaattttggtaaaagccccaggttatccatggtagccgcttgcactgagacgaaagaaactaaggat
agtttgaactactaatagctcatttaagtcttataaagggttttggtttctcctgactcaattttgcatgggtgaaaag
aaataggttaagccattattggattccgaaatagccaaatttctgggttcctcaagcggaagctcaaaagaaactattg
aagcttatgggcttcaaaaactcctcctgatttaaaggaggaaatctccaccgatgggaaatgggatatgcttatcagct
gctgagggaagcctaatttttgcaaaaaagaaaatatcatctgggagacatctcttgatgaatcagatgaggagaglat
ctccagggatccttgatgtcaataacttctatttctgaaatgtatgggtcctactgtcgcttcgacttctcgtagctcta
cgcagttaagtgaccaaaaggtacc

FIG. 30
(CONTINUED)

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FIG. 31

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
 S-2: RQH LKR VQL RDV SEA EVR QHR EA
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YV

FIG. 32

Poly 4
 t a a g c c t c g
 5'- cag acc aaa gga att cca taa gg -3'
 Q T K G I P Q G

4(B')

5(c')
 D D Y L L I T
 3'- ctg ctg atg gag gag tag tgg -5'
 a a a a a a a a
 t t t t
 c c
Poly 1

FIG. 34

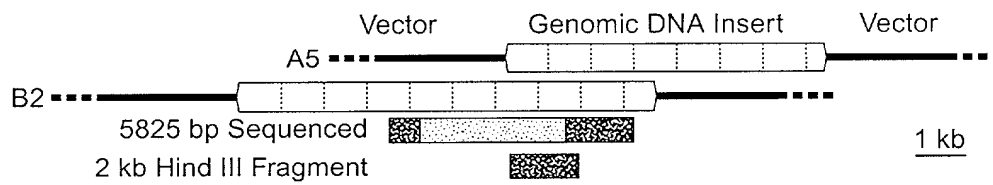


FIG. 33A

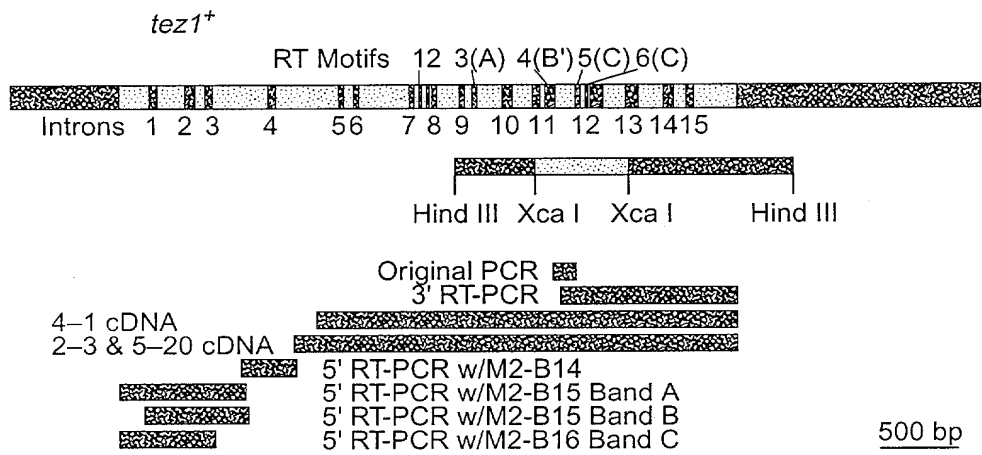


FIG. 33B

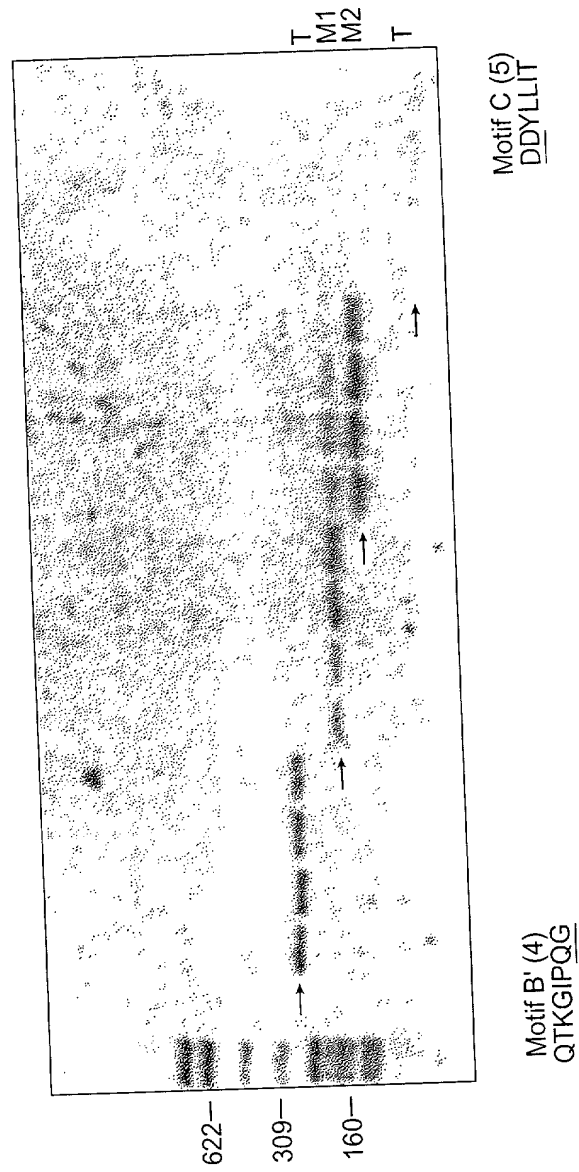


FIG. 35

[illegible]

FIG. 36

GAT GAT TTT ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT
 E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
 CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

<----- ctg ctg atg gag gag tag tgg
 a a a a a a a t t t
 t t t t t t t t t t
 C C C C C C C C C C

Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence
 D D F L F I T

FIG. 36
 (CONTINUED)

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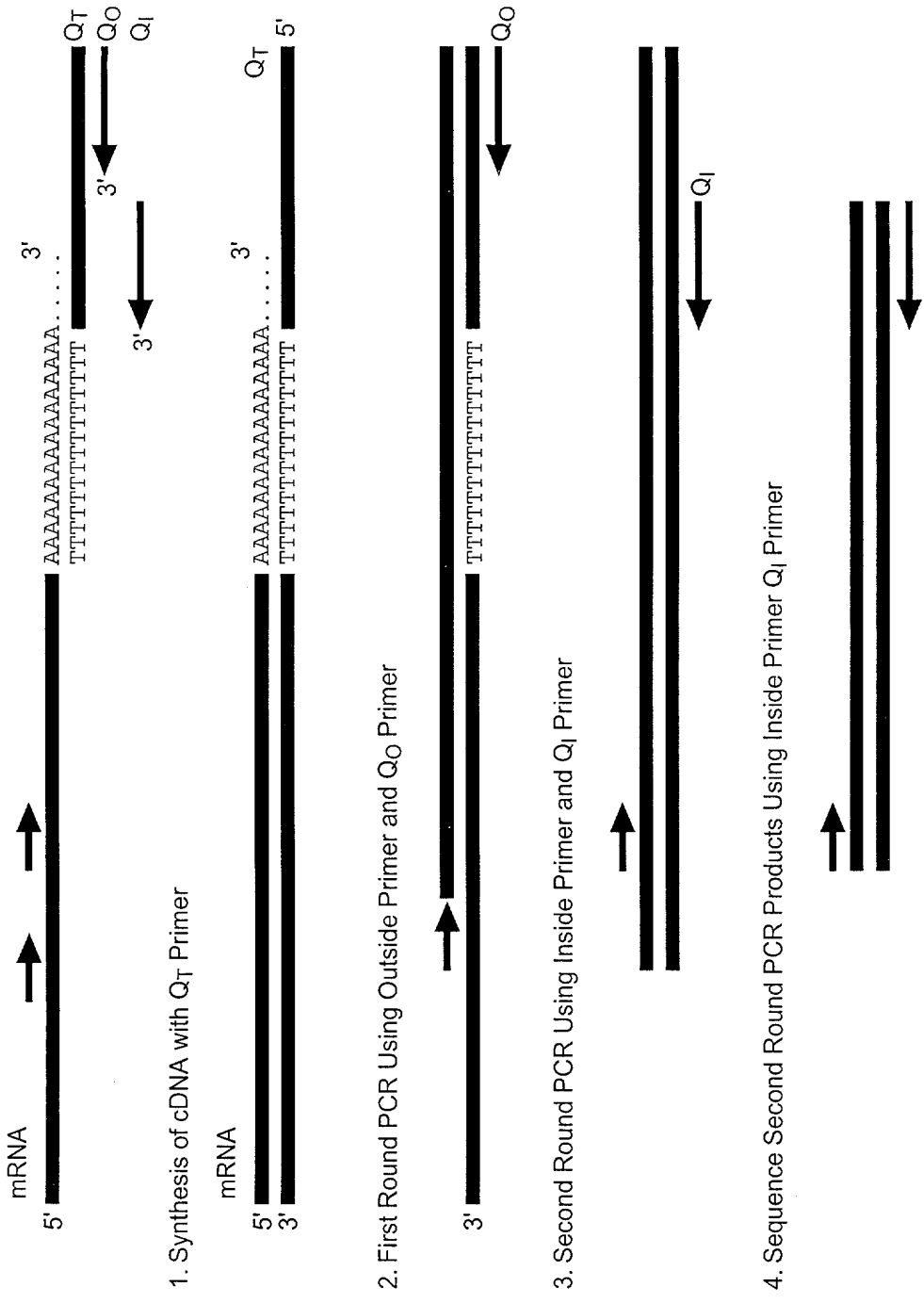


FIG. 37

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- A. Genomic Libraries**
- Size Selected Libraries from P. Nurese
 - 3~4 kb
 - 5~7 kb
 - 7~8 kb
 - 11~12 kb
 - Libraries from J.A. Wise
 - Sau 3a Partial Digest
 - Hind III Partial Digest
- cDNA Libraries**
- GAD (Gal Activation Domain) Library
 - REP Library from R. Allshire
 - REP81ES Library (old)
 - REP81ES Library (new)
 - REP41ES Library

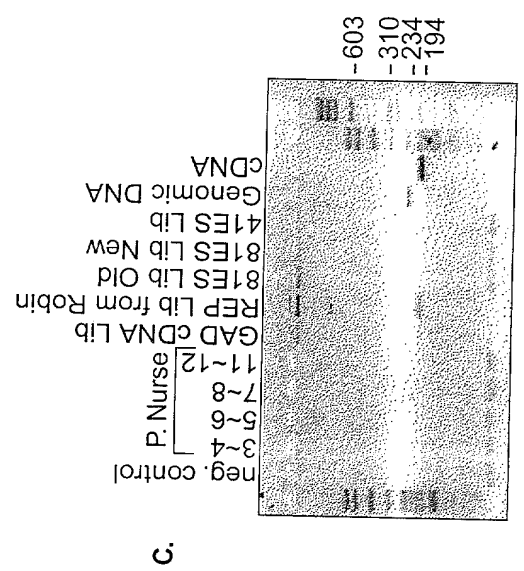
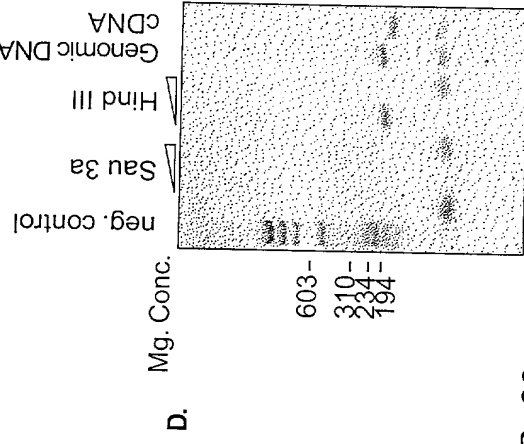
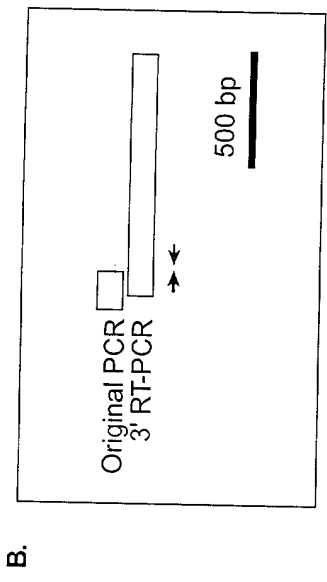


FIG. 38

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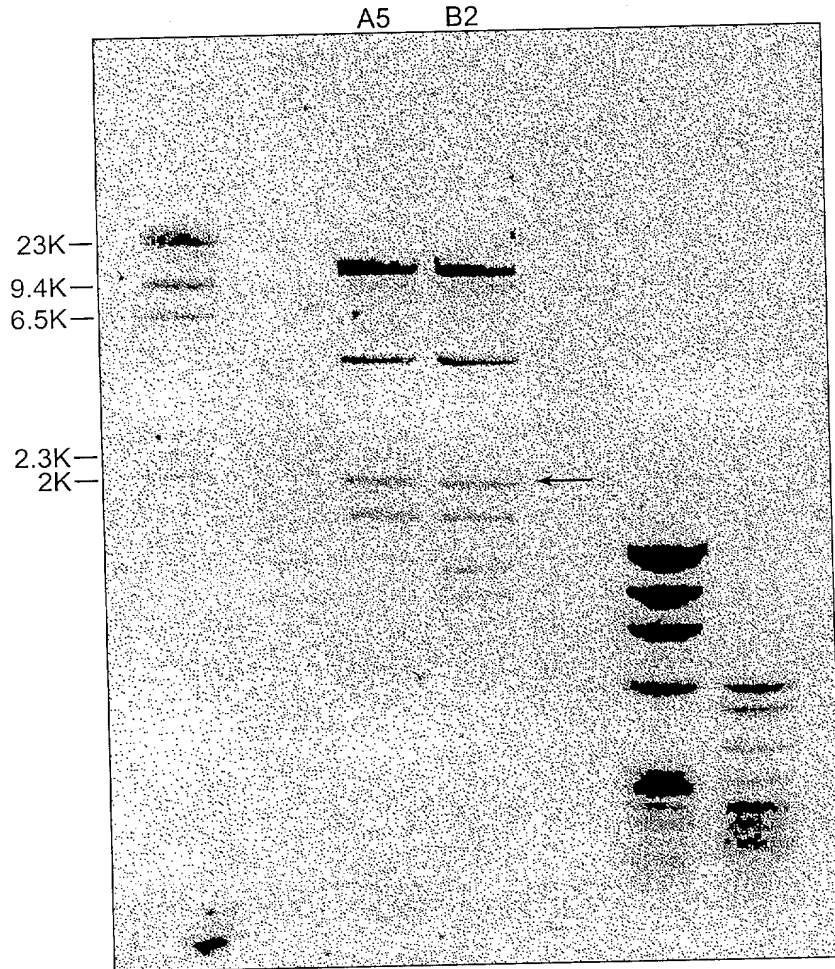


FIG. 39

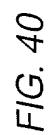


FIG. 40

Motif O

S.p. Tez1p	(429) . WLYNSFIIPILQSFYITESSDLNRRTVYFRKDIW	... (35) ...
S.c. Est2p	(366) . WLFRLIPKIIQTFFYCTEISSTVT-IVYFRHDTW	... (35) ...
E.a. p123	(441) . WIFEDLVVSLIRCFYVTEQQKSYKTYYYRKNIW	... (35) ...
	*** ** *	
	Motif 1 Motif 2 K	
	p hh h K hr h R	
S.p. Tez1p	AVIRLLPKK--NTFRLITN-LRKRF	... (61) ...
S.c. Est2p	SKMRIIPKKSNEFRIIAPCRGAD	... (62) ...
E.a. p123	GKLRLLPKK--TTFRPIMTFNKKIV	... (61) ...
	* *** ** *	
	Motif 3(A) AF	
	h hDh GY h	
S.p. Tez1p	KKYFVRIDIKSCYDRIKQDLMFRIVK	... (89) ...
S.c. Est2p	ELYFMKFDVKSCYDSIPRMECMRILK	... (75) ...
E.a. p123	KLFFATMDIEKCYDSVNREKLSTFLK	... (107) ...
	* * *** *	
	Motif 4(B')	
	hPQG pP hh h	
S.p. Tez1p	YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF	... (6) ...
S.c. Est2p	YIREDLGFQGSLSAPIVDLVYDDLLEFYSEF	... (8) ...
E.a. p123	YKQTKGIPQGLCVSSILSSFYATLEESSLGF	... (14) ...
	* * * * *	
	Y Motif 5(C)	
	h F DDh hh	
S.p. Tez1p	VLLRVVDDFLFITVVKKDAKKFLNLSRGFEKHNFSTLEKTVINFENS	... (205)
S.c. Est2p	LILKLADDFLIISTDQQQVINIKLAMGGFQYNAKAPDKILAVSSQS	... (173)
E.a. p123	LLMRLTDDYLLITTTQENNAVLFIKFLINVSRENGFKFNMKKIQTSFFLS	... (209)
	** * * *	
	Motif 6(D)	
	Gh h ck h	

FIG. 41

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A.			
Sp_Tip1p	1	-----MTEHHTPKSRILRFLENQYVYLCT	24
Sc_Est2p	1	-----MTEHHTPKSRILRFLENQYVYLCT	7
Ea_p123	1	MEVDVDNQADNHGISHALKTCEEIKEAKTLYSW	33
Sp_Tip1p	25	LNDYVQLVLRGSPA[SY]SNIC[ER]LRSDVQTSFS	57
Sc_Est2p	8	IQDKLDIDLQTN--S[TYK]--E[EN]LKC[GH]FNGLD	35
Ea_p123	34	IQKVI[RCRN]QSQ--S[HYK]--DLEDIKIFAQTN	61
Sp_Tip1p	58	[I]F[L]HSTVVGFD[SK]PDEGVQFSSPKCS[Q]S[EL]IAN	90
Sc_Est2p	36	EIL[T]TCFALPNSR-KIALPCLPGDLS[SH]KAVIDH	67
Ea_p123	62	[I]VATPRDYNEEDFKV[IA]RKEVFSTGLMIE[EL]IDK	94
Sp_Tip1p	91	VVKQMFDES[FERR]-NLLMKGF[SM]NHEDFRAMH	122
Sc_Est2p	68	CIIYLLTGELYN--NVLTFGYK[IA]RNEDE--	93
Ea_p123	95	CLVELLSSSDVSDR[QKL]QC[F]G[F]QLKGNQ--	122
Sp_Tip1p	123	VNGVQNDL[VST]FPN[YL]ISIL[ES]KNWQLLEIIG	155
Sc_Est2p	94	--VNN[SL]FCHSANVNVTL[LL]KGAAWKMFHSLVG	123
Ea_p123	123	--LAKTHLLTALSTQKQYFFQDEWNQVRAMIG	152
Sp_Tip1p	156	SDAMHYLL[SK]GSIF[EAL]PNDNYL[QISG]IPL[F]KN	188
Sc_Est2p	124	TYAFVDLLIN[YT]VIQFN-GQFFTQIVGNRCNEP	155
Ea_p123	153	NELFRHLYTKYLIFQRTSEGTLVQFCGNNVF[FDH]	185
Sp_Tip1p	189	NVFEETV[SK]KR[KRT]IET[IT]QN--K[SAR]KE[VS]	218
Sc_Est2p	156	HLPPKWVQ--R[SSSS]SA[TAAQ]I--K[QL]TEPVT	183
Ea_p123	186	LKVNDKFDK-KQKGGAA[DM]NEPRCCSTCKYNVK	217

FIG. 42

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A.

Sp_Tip1p	219	WNSISISRSFSIFYSRSSYKFKKQDL	YFN	LH	SI	CD	251
Sc_Est2p	184	N-----KQFLHKL	N	IN	SS	FF	200
Ea_p123	218	NEK--DHFLNNINVPNWNMMKSRTR	I	F	Y	CTHFN	248
Sp_Tip1p	252	RNTVHMWLQWIFPRQFGLINAFQVKQL	L	HK	VI	PL	284
Sc_Est2p	201	-----YSKIL	LPSS	--S	IKKL	TDL	223
Ea_p123	249	R-----NNQFF	EKKHEFVSN	KNN	I	SAMDRAQTI	275
Sp_Tip1p	285	VS-----QSTVVP	KRL	LKV	YPL	IEQTAKR	313
Sc_Est2p	224	TN-----LVKI	PQR	LKV	RIN	TLQKL	252
Ea_p123	276	FTNIFRFNRIRKKL	KDKV	IEK	IAYML	EKV	308
Sp_Tip1p	314	LSKVYNHYCPYID	-THDD	EKIL	SYSL	KPNQ	342
Sc_Est2p	253	YVSI	LNSICP	PLE	EGT	VL	282
Ea_p123	309	FNYYL	TKSC	PLPEN	WRER	KQKIEN	341
Sp_Tip1p	343	-----VF	FLRS	I	L	VRV	359
Sc_Est2p	283	-----VL	KFI	I	V	L	299
Ea_p123	342	SKYYEEL	FSYTTDNKCV	TQF	I	NEFFYN	374
Sp_Tip1p	360	WGNQR	I	FEI	I	L	392
Sc_Est2p	300	FGSK	KNK	GK	I	KN	332
Ea_p123	375	LTG	-RNR	KNFQ	K	VKKYVEL	406
Sp_Tip1p	393	N	I	K	I	S	425
Sc_Est2p	333	K	L	R	L	K	362
Ea_p123	407	K	I	N	T	R	437

FIG. 42
(CONTINUED)

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A.	Sp_Tip1p	426	E	F	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	T	V	Y	458
	Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	I	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394
	Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	V	S	L	I	R	C	F	F	Y	V	T	E	Q	Q	K	S	Y	S	K	T	Y	Y	470
	Sp_Tip1p	459	F	R	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491
	Sc_Est2p	395	F	R	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	F	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427
	Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503
	Sp_Tip1p	492	T	Q	K	T	T	L	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522	
	Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460
	Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	K	I	V	534
	Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	-	552
	Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	T	491
	Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564	
	Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
	Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
	Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	597
	Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616
	Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
	Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
	Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
	Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570	
	Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	N	I	V	I	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663

FIG. 42

(CONTINUED)

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A.	Sp_Tip1p	635	F	V	S	E	A	F	S	Y	F	D	M	V	P	F	E	K	V	V	Q	L	L	S	-	-	M	K	T	S	D	T	L	F	V	665				
	Sc_Est2p	571	-	-	-	-	-	-	-	-	-	-	-	V	L	K	L	F	N	V	V	N	A	S	R	-	-	V	P	K	P	Y	E	L	Y	I	591			
	Ea_p123	664	F	Q	K	I	A	L	E	G	G	Q	Y	P	T	L	F	S	V	L	E	N	E	Q	N	D	L	N	A	K	K	T	L	I	V	696				
	Sp_Tip1p	666	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	K	M	L	K	E	H	L	S	G	H	I	V	K	I	G	N	S	Q	Y	698				
	Sc_Est2p	592	D	N	V	R	T	V	H	L	S	N	Q	D	V	I	N	V	V	E	M	E	I	F	K	T	A	L	W	V	E	D	K	C	Y	624				
	Ea_p123	697	E	A	K	Q	R	N	Y	F	K	K	D	N	L	L	Q	P	V	I	N	I	C	Q	Y	N	Y	I	N	F	N	G	K	F	Y	729				
	Sp_Tip1p	699	L	Q	K	V	G	I	P	Q	G	S	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	F	T	K	731				
	Sc_Est2p	625	I	R	E	D	G	L	F	Q	G	S	S	L	S	A	P	I	V	D	L	V	Y	D	D	L	L	E	F	Y	S	E	F	K	A	657				
	Ea_p123	730	K	Q	T	K	G	I	P	Q	G	L	C	V	S	S	I	L	S	S	F	Y	Y	A	T	L	E	E	S	S	L	G	F	L	R	762				
	Sp_Tip1p	732	K	K	G	-	-	-	-	-	-	-	-	-	-	-	-	-	S	V	L	L	R	V	V	D	D	F	L	F	I	T	V	N	K	K	D	A	K	756
	Sc_Est2p	658	S	P	S	Q	D	-	-	-	-	-	-	-	-	-	-	-	T	L	I	L	K	L	A	D	D	F	L	I	I	S	T	D	Q	Q	V	I	N	684
	Ea_p123	763	D	E	S	M	N	P	E	N	P	N	V	N	L	L	M	R	L	T	D	D	Y	L	L	I	T	T	Q	E	N	N	A	V	L		795			
	Sp_Tip1p	757	F	L	N	L	S	L	R	G	F	E	K	H	N	F	S	T	S	L	E	K	T	V	I	N	F	E	N	S	N	G	-	-	-	-	-	786		
	Sc_Est2p	685	I	K	K	L	A	M	G	G	F	Q	K	Y	N	A	K	A	N	R	D	K	I	L	A	V	S	S	Q	S	D	-	-	-	-	-	-	713		
	Ea_p123	796	F	I	E	K	L	I	N	V	S	R	E	N	G	F	K	F	N	M	K	K	L	Q	T	S	F	P	L	S	P	S	K	F	A		828			
	Sp_Tip1p	787	-	-	-	I	I	N	N	T	F	F	N	E	S	K	K	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L		816			
	Sc_Est2p	714	-	-	-	D	D	T	V	I	Q	F	C	A	-	-	-	M	H	I	F	V	K	E	L	E	V	W	K	H	S	S	T	M		739				
	Ea_p123	829	K	Y	G	M	D	S	V	E	E	Q	N	I	V	Q	D	Y	C	D	W	I	G	I	S	I	D	M	K	T	L	A	L	M	P		861			
	Sp_Tip1p	817	A	C	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	K	S	F	F	Y	K	I	L	R	S	S		849			
	Sc_Est2p	740	N	N	F	H	I	R	S	K	S	S	K	G	I	F	R	S	L	I	A	L	F	N	T	R	I	S	Y	K	T	I	D	T	N		772			
	Ea_p123	862	N	I	N	L	R	I	E	G	I	L	C	T	L	N	L	N	M	Q	T	K	K	A	S	M	W	L	K	K	L	K	S	F		894				

FIG. 42
(CONTINUED)

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A.

Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882					
Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	-	793				
Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927					
Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	K	915					
Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821					
Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960					
Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948					
Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854					
Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993					
Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981					
Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	Y	877					
Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	T	K	K	Y	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K	L	K	S	D	Q	C	1023
Sp_Tip1p	982	L	H	R	R	I	A	D	-																											988				
Sc_Est2p	878	I	Y	I	H	I	V	N	-																											884				
Ea_p123	1024	Q	S	L	I	Q	Y	D	A																											1031				

FIG. 42
(CONTINUED)

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B.			
Sp_Tip1p	1	-----MTEHHTPKSRILRFLENQYVYLCT	24
Sc_Est2p	1	-----MKILFEF	7
Ea_p123	1	MEVDVDNQADNHGHSALKTCEEIKEAKTLYSW	33
Sp_Tip1p	25	LNDYVQLVLRGSPA	57
Sc_Est2p	8	IQDKLDIDLQTN--STYK--ENLKCGHFNGLD	35
Ea_p123	34	IQKVIRCRNQSQ--SHYK--DLEDIKIFAQTN	61
Sp_Tip1p	58	IFLHSTVVGFDSPKDEGVQFSSPKCSQSEL	90
Sc_Est2p	36	EILTTCFALPNSR-KIALPCLPGDLSHKAV	67
Ea_p123	62	I V A T P R D Y N E E D F K V I A R K E V F S T G L M I E L I D K	94
Sp_Tip1p	91	VVKQMFDESFERRR-NLLMKGF	122
Sc_Est2p	68	CIIYLLTGELYN--NVLTFFGYK IARNED--	93
Ea_p123	95	CLVELSSSDVSDRQKLQCFGF	122
Sp_Tip1p	123	VNGVQNDLVSTFPNYLISILESKN	155
Sc_Est2p	94	--VNNSLFCHSANVNVTLLKGAAWKMFHSLVG	123
Ea_p123	123	--LAKTHTLLTALSTQKQYFFQDEWNQVRAMIG	152
Sp_Tip1p	156	SDAMHYLLLSKGSIFEALPNDNYLQ	188
Sc_Est2p	124	TYAFVDLLINYYTVIQFN-GQFFFTQIVGNRCNEP	155
Ea_p123	153	NELFRHL YTKYLI FQRTSEGTLVQFCGNNVFDH	185
Sp_Tip1p	189	NVFEETVSKKRKRTIETSI TQN--KSARK	218
Sc_Est2p	156	HLPPKWVQ--RSSSSSATAAQI--KQLTEPVT	183
Ea_p123	186	LKVNDKFDK-KQKGGGAADMNEPRCCSTCKYNVK	217

FIG. 42

(CONTINUED)

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[illegible]

FIG. 42
(CONTINUED)

B.	Sp_Tip1p	426	EF	I	Y	W	L	Y	N	S	F	I	P	I	L	Q	S	FF	Y	I	T	E	S	S	D	L	R	N	R	T	V	Y	458			
	Sc_Est2p	363	CF	I	S	W	L	F	R	Q	L	I	P	K	I	I	Q	T	FF	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394		
	Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	S	L	I	R	C	FF	Y	V	T	E	Q	Q	K	S	Y	S	K	T	Y	Y	470		
	Sp_Tip1p	459	FR	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491	
	Sc_Est2p	395	FR	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	F	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427	
	Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503
	Sp_Tip1p	492	T	Q	K	T	T	L	P	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522
	Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460
	Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	K	I	V	534
	Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	-	552
	Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	T	491
	Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564	
	Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
	Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
	Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	597
	Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616
	Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
	Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
	Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
	Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570	
	Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	N	I	V	I	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663

FIG. 42
(CONTINUED)

B.		
Sp_Tip1p	635	FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV 665
Sc_Est2p	571	-----VLKLFNVVNASR--VPKPYELI 591
Ea_p123	664	FQKIALEGGQYPTLFSVLENEQNDLNAKKTII 696
Sp_Tip1p	666	DFVDYWTKSSSEIFKMLKEHLSGHI VKIGNSQY 698
Sc_Est2p	592	DNVRTVHLSNQDVINVVEMEIEFKTALWVEDKCY 624
Ea_p123	697	EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY 729
Sp_Tip1p	699	LQKVGI PQGSILS SFLCHFYMEDL IDEYLSFTK 731
Sc_Est2p	625	IREDGLFQGSLSAPIVDLVYDDL LEFYSEFFKA 657
Ea_p123	730	KQTKGIPQGLCVSSILSSFYATLEEESLGFELR 762
Sp_Tip1p	732	KKG-----SVLLRVVDDFLFI TVNKKDAKK 756
Sc_Est2p	658	SPSQD-----TLILKLADDFLIISTDQQQVIN 684
Ea_p123	763	DESMNPENPNVNLLMRLTDDYLLIT TQENNAVL 795
Sp_Tip1p	757	FLNLSLRGFEKHNFSTLEKTVINFENSG-- 786
Sc_Est2p	685	IKKLAMGGFQKYNAKANRDKILAVSSQSD-- 713
Ea_p123	796	FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA 828
Sp_Tip1p	787	---IINN TFFNESKKRMPFFGFSVNMRSLDTLL 816
Sc_Est2p	714	---DDTVIQFCA--MHIFVKELEVWKHSSSTM 739
Ea_p123	829	KYGMDSVEEQNI VQDYCDWIGISIDMKTLALMP 861
Sp_Tip1p	817	ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS 849
Sc_Est2p	740	NNFHIRSKSSKGI FRSLIALFNTRISYKTIDTN 772
Ea_p123	862	NINLRIEGLCTLNLMQTKKASMWLKKKLSF 894

FIG. 42
(CONTINUED)

B.

Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882
Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	793
Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927	
Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	915	
Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821
Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960
Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948
Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854
Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993
Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981
Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	Y	877
Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	T	K	K	Y	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K	1023	
Sp_Tip1p	982	L	H	R	R	I	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988		
Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884		
Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031		

FIG. 42
(CONTINUED)

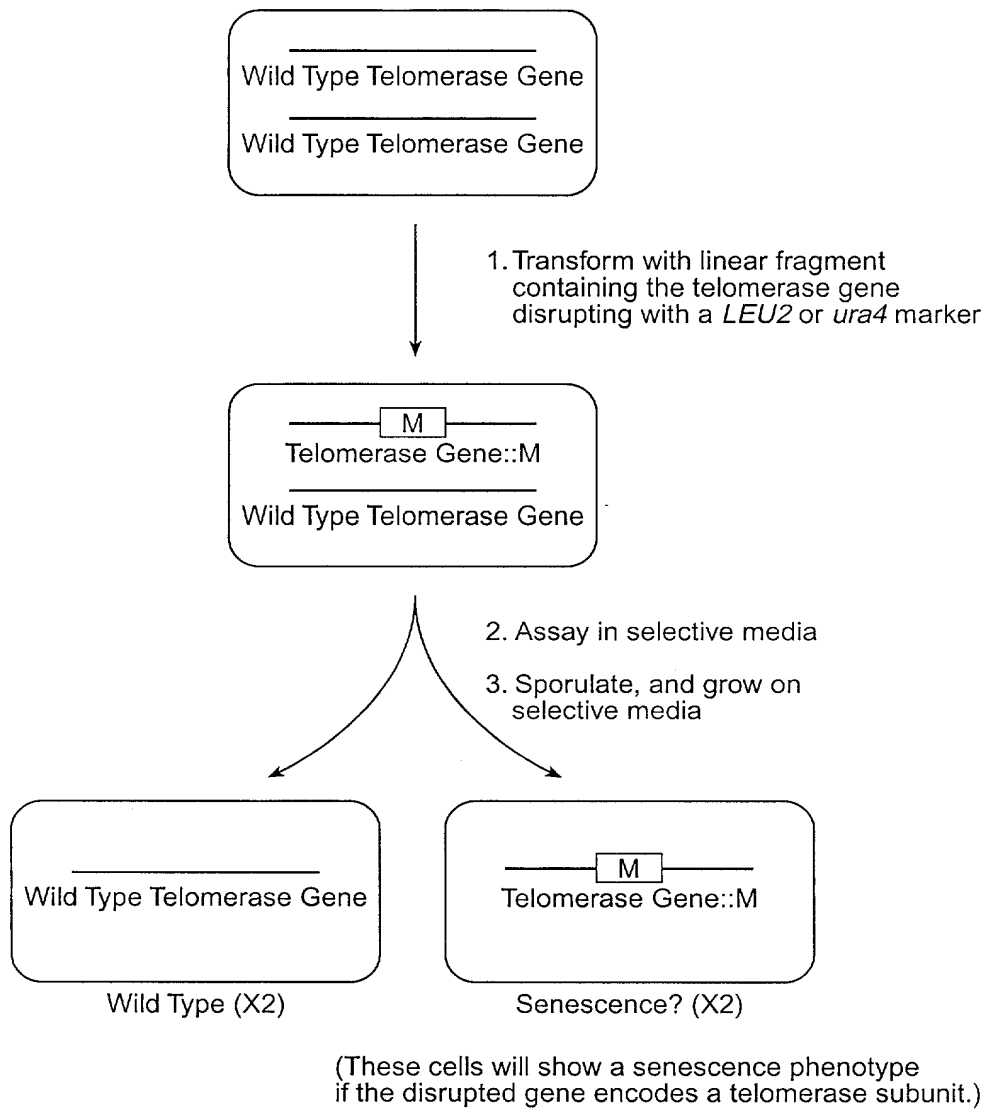
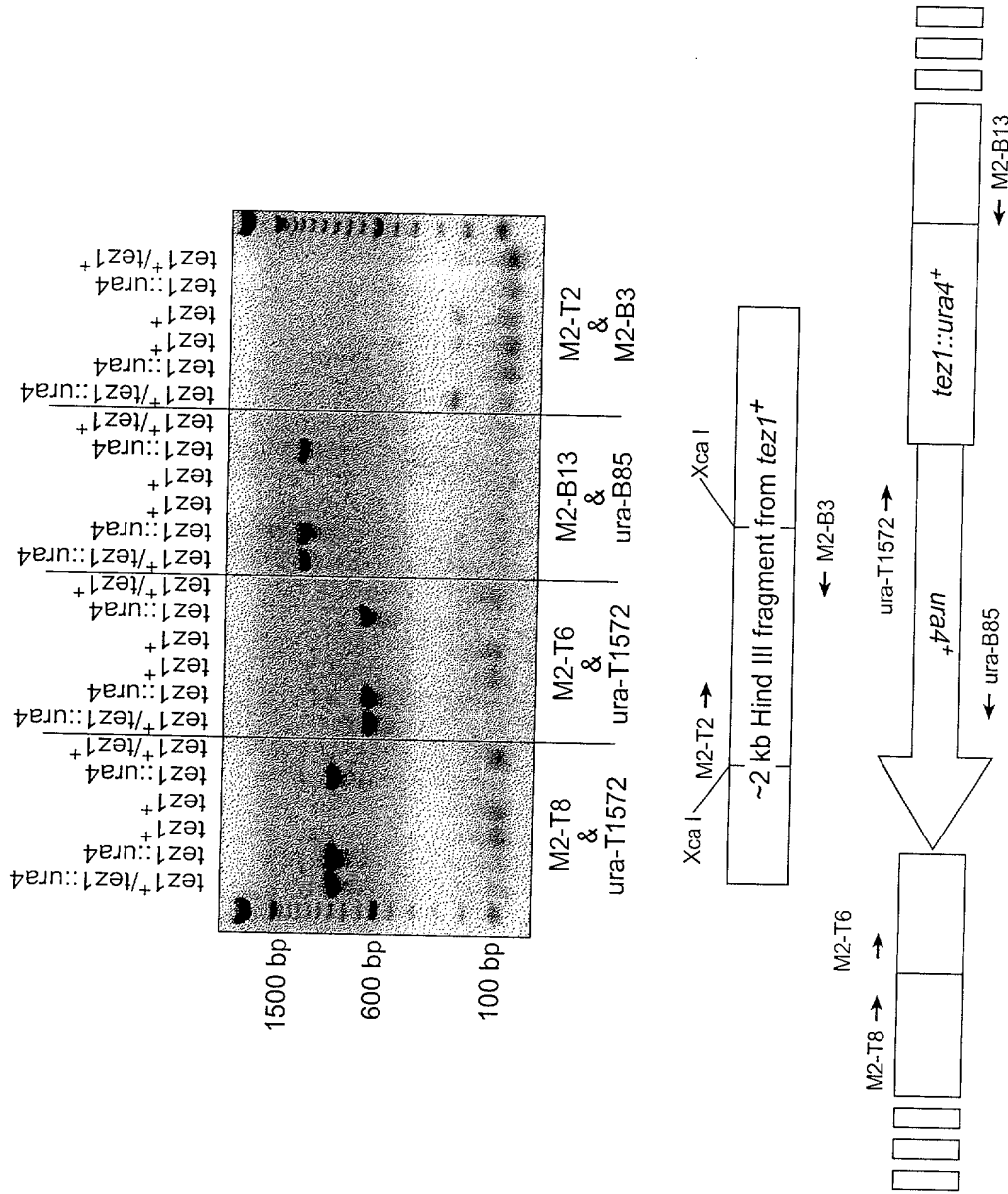


FIG. 43



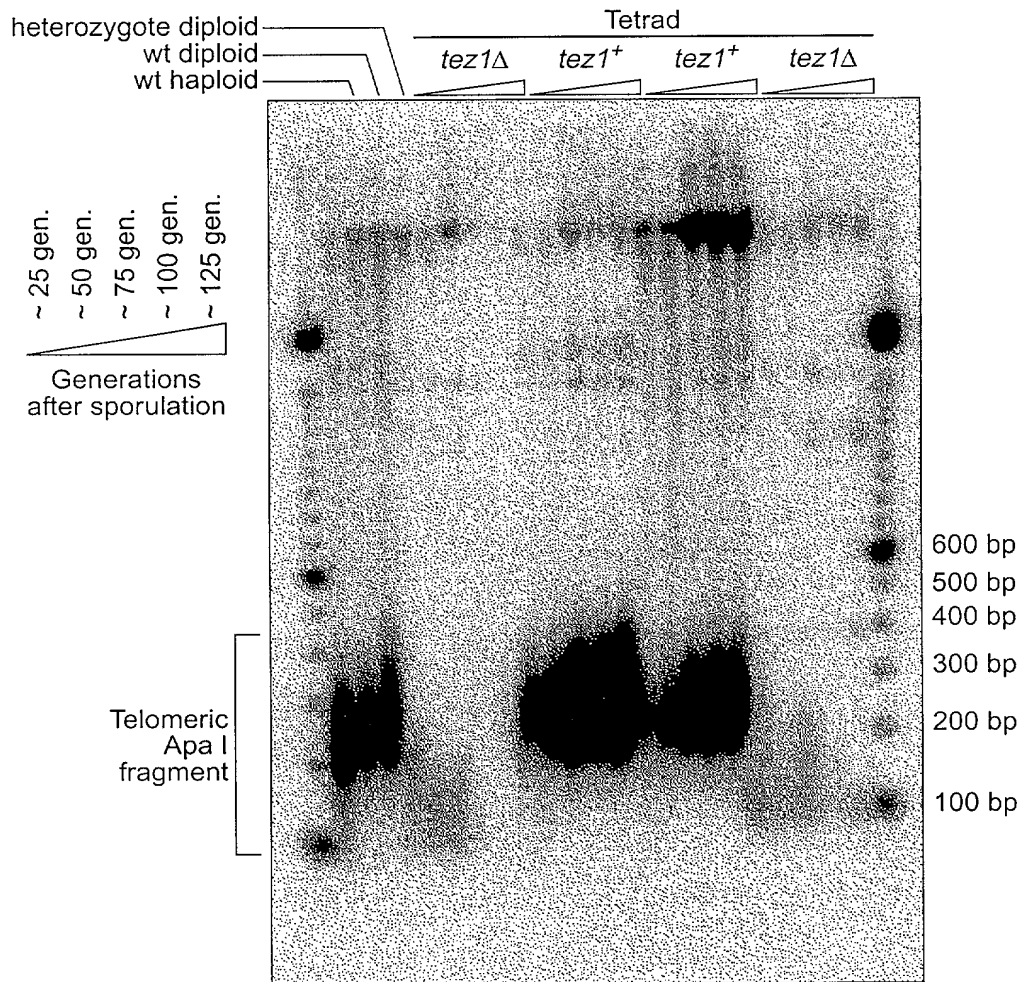


FIG. 45

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FIG. 46

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1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D L V S T F P N Y L I S I L E S K N W Q 148
 1530 CTT TTG TTA GAA AT gtaaataccgggtaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L L L E I I G 155
 1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S D A M H Y L L S K G S I F E A L P N D 175
 1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N Y L Q I S G I P L F K N N V F E T V 195
 1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
 196 S K K R K R T I E T S I T Q N K S A R K 215
 1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E V S W N S I S I S R F S I F Y R S S Y 235
 1842 AAG AAG TTT AAG CAA G gtaactaataactgtttactcttcataactaatttag AT CTA TAT TTT AAC 1907
 236 K K F K Q D L Y F N 245
 1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L H S I C D R N T V H M W L Q W I F P R 265
 1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
 266 Q F G L I N A F Q V K Q L H K V I P L V 285
 2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S Q S T V V P K R L L K V Y P L I E Q T 305
 2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A K R L H R I S L S K V Y N H Y C P Y I 325
 2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D T H D D E K I L S Y S L K P N Q V F A 345
 2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
 346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 46

(CONTINUED)

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2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F E I I L K D L E T 375
 2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
 376 F L K L S R Y E S F S L H Y L M S N I K 395
 2397 gtaatatgccaaattttttaccattaataacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
 396 I S E I E W L V L G 405
 2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
 406 K R S N A K M C L S D F E K R K Q I F A 425
 2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445
 2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
 446 I T E S S D L R N R T V Y F R K D I W K 465
 2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705
 466 L L C R P F I T S M K M E A F E K I N E 485
 2706 gtattttaaaagtatttttgcacaaagctaattttccag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486 N N V R M D T Q K T 495
 2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
 496 T L P P A V I R L L P K N T F R L I T 515
 2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaaatttttggtcatcaatgtactttacttctaattatta 2906
 516 N L R K R F L I K 524
 2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT AGC AAC CAA ACT TTA CGA CCT GTG 2967
 525 M G S N K K M L V S T N Q T L R P V 542
 2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
 543 A S I L K H L I N E S S G I P F N L E 562
 3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaaat 3088
 563 V Y M K L L T F K D L L K H R M F G 581

FIG. 46

(CONTINUED)

FIG. 46
 (CONTINUED)

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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TAC AAA ATT CTA AG gtatactgtgaactgaataatagctgacaaaataacag A TCG 4089
839 K S F F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889 R M K D I F I P Q R M F I T D 903

4275 aaagtcattaattaacaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904 L L N V I G R K I W K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E I L G Y T S R R F L S S A E V K W 935

4402 ggtctcgagacttcagcaaatattgacacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588
967 D L I K P L R P V L R Q V L F L H R R I 986

4589 GCT GAT TAA tgtcattttcaatttatttatatacatccttttattactggtgtcttaacaataattattactaagtata 4665
987 A D * 989

FIG. 46
(CONTINUED)

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4666 gctgacccccaaagcagcatactataggatttcctagtaaagtaaaattaatctcgttatttagttttagtgcattgtct 4745
 4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgccacatgccattaaacgggagtggttaaaca 4825
 4826 ttaaaagtaatacatgaggctaattccttctcatttagaataaggaagtggttttctataatgaataatgccgcacta 4905
 4906 atgcaaaaaagacgaagattatcttcaacaaggggattaaagcatatccgaaggaaaagagagtaatataccagtggt 4985
 4986 gtggaagaaagcaaggataaatttggaaacaagcttctgcagatgacaggtcaaatcttggtgacggaatttggtaaaagc 5065
 5066 cccagggttatccatggtggtggccgcttgctactgagacgaaagaaactaaggatagtttgaataactaatagctcattta 5145
 5146 atgtcttataaaggttttggtttctcctgactcaatttgcattgggtgaaagaaatagtttaagccattattggat 5225
 5226 tccgaaatagccaaatttcttggttctcctcaagcgggaagtcaaaagaacttatgaagcttatgaggcttcaaaaactcc 5305
 5306 tcttgatttaaaggaggaatcttccaccgatgggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385
 5386 aaaaagaaaaatctattgggagacatctcttgatgaatcagatcggagagtatctccagcggatccttgatgtcaata 5465
 5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagtttaagtgaacaaaggtagc 5544

FIG. 46
(CONTINUED)

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1
 GCCAAGTTCCTGCACTGGCTG met ser val tyr val val glu leu leu
 ATG AGT GTG TAC GTC GTC GAG CTG CTC

10 20
 arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
 AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

30
 leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
 CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40 50
 gly ile arg gln his leu lys arg val gln leu arg glu leu ser
 GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

60
 glu ala glu val arg gln his arg glu ala arg pro ala leu leu
 GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

70 80
 thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
 ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

90
 ile val asn met asp tyr val val gly ala arg thr phe arg arg
 ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100 110
 glu lys ala glu arg leu thr ser arg val lys ala leu phe
 GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

120
 ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
 AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130 140
 ala ser val leu gly leu asp asp ile his arg ala trp arg thr
 GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

150
 phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
 TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160 170
 phe val lys val asp val thr gly ala tyr asp thr ile pro gln
 TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

180
 asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
 GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190 200
 thr tyr cys val arg arg tyr ala val val gln lys ala ala met
 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

FIG. 47

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210
 gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
 GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220 230
 gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
 CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

240
 leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
 CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250 260
 arg asp gly leu leu leu arg leu val asp asp phe leu leu val
 CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

270
 thr pro his leu thr his ala lys thr phe leu arg thr leu val
 ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280 290
 arg gly val pro glu tyr gly cys val val asn leu arg lys thr
 CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

300
 val val asn phe pro val glu asp glu ala leu gly gly thr ala
 GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310 320
 phe val gln met pro ala his gly leu phe pro trp cys gly leu
 TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

330
 leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
 CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340 350
 tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
 TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

360
 phe lys ala gly arg asn met arg arg lys leu phe gly val leu
 TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370 380
 arg leu lys cys his ser leu phe leu asp leu gln val asn ser
 CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

390
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

FIG. 47
(CONTINUED)

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420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC
AGGCTGGCGTTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTGTTTACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 47
(CONTINUED)

Motif -1
 Ep p123 ...LVVSLIRCFYVTEQQKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESSDLRNRT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRLLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPPIPAVIRLLPKKN--TFRLITNLRKRFL...
 Sc Est2 ...TLSNFNHSMRIIPKKSNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPVNMMDYVVG...
 consensus R PK R I

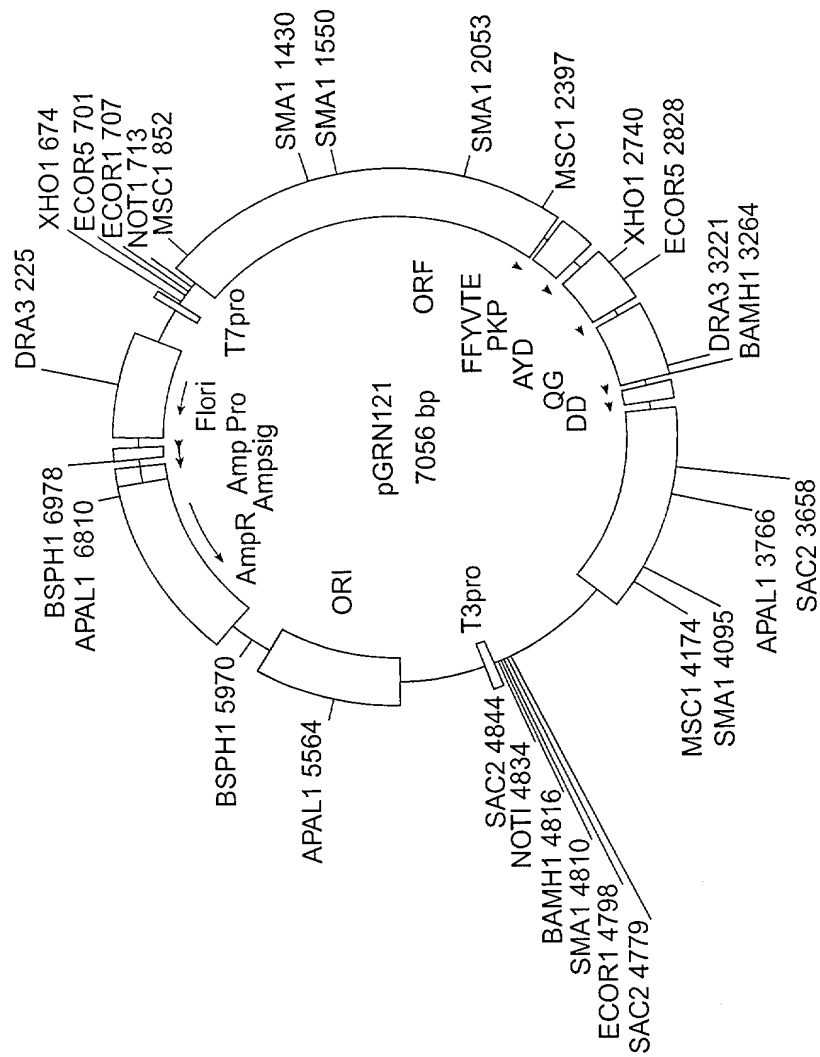
Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFYKQTKGIPQGGLCVSSILSSFYFA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFEEKHNFST...
 Sc Est2 ...KKLAMGGFQKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

FIG. 48



1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCCGCG GGGGCCCCCC CGAGGCCTTC
 401 ACCACCAGCG TGCAGAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGG TGCGCGNTNT TTGTGCTGGT GGNTCCAGC
 551 TGCGCCTACC ANGTGTGCGG CCGCGCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCCG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGCG AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGEC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCTCTAC
 1051 TCCTCAGGCG ACAAGNACAT TCGNCCCTC CTTCTACTC AATATATCTG
 1101 AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
 1201 GCGNACTTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGAACACG
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTACACC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCCTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCAGACGAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCCTGCGC CCGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
 1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTGCGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCACTGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC
 2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
 2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
 2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
 2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCTA CGTTTCATGT GCCACCACGC

FIG. 50

2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601 AACAACTGTG TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCCTTTGGT
2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701 TCAGGACCCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGGCCTGC
2851 TGCTGGATAC CCGGACCCCT GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCAACA
3001 GCCTGTTTCT GGATTTGTCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCACCA TTTTTCCTGC
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
3251 CGAGGCCCGT CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACCTAG GACAGCCCAG
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601 CCGGCTGAAG GCTGAGTGTG CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCTT CACCAGGAGC CCGGCTTCCA
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIG. 50
(CONTINUED)

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GCAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC
1  -----+-----+-----+-----+-----+-----+ 60
CGTCGCGACGCAGGACGACGCGTGCACCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG

a  A A L R P A A H V G S P G P G H P R D A -
b  Q R C V L L R T W E A L A P A T P A M P -
c  S A A S C C A R G K P W P R P P P R C R -

GCGCGCTCCCCGCTGCCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
61  -----+-----+-----+-----+-----+ 120
CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGA

a  A R S P L P S R A L P A A Q P L P R G A -
b  R A P R C R A V R S L L R S H Y R E V L -
c  A L P A A E P C A P C C A A T T A R C C -

GCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
121  -----+-----+-----+-----+-----+ 180
CGCGGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCAGCCGCCGACCAGTTCGCGCC

a  A A G H V R A A P G A P G L A A G A A R -
b  P L A T F V R R L G P Q G W R L V Q R G -
c  R W P R S C G A W G P R A G G W C S A G -

GGACCCGGCGGCTTTCGCGCGNTGGTGGCCANTGCNTGGTGTGCGTGCCCTGGGANGN
181  -----+-----+-----+-----+-----+ 240
CCTGGGCGCGGAAAGGCGCGNACCACCGGTNACGNACCACACGCACGGGACCCTNCN

a  G P G G F P R ? G G P ? ? G V R A L G ? -
b  D P A A F R A ? V A ? C ? V C V P W ? ? -
c  T R R L S A R W W P ? A W C A C P G ? ? -

ANGGCNGCCCCCGCGCCCCCTCCTTCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC
241  -----+-----+-----+-----+-----+ 300
TNCCGNCGGGGGGCGCGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG

a  ? A A P R R P L L P P G V L P E ? ? G G -
b  ? ? P P A A P S F R Q V S C L ? ? L V A -
c  G ? P P P P P P S A R C P A * ? ? W W P -

CCGAGTGCTGCANANGCTGTGCGANCGCGGCGGAANAACGTGCTGGCCTTCGGCTTCGC
301  -----+-----+-----+-----+-----+ 360
GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTTNTGACGACCGGAAGCCGAAGCG

a  P S A A ? A V R ? R R E ? R A G L R L R -
b  R V L ? ? L C ? R G A ? N V L A F G F A -
c  E C C ? ? C A ? A A R ? T C W P S A S R -

GCTGCTGGACGGGGCCCGCGGGGCCCCCCCCGAGGCCTTCACCACCAGCGTGCAGCTA
361  -----+-----+-----+-----+-----+ 420
CGACGACCTGCCCCGGGCGCCCCCGGGGGGCTCCGGAAGTGGTGGTTCGACGCGTCGAT

a  A A G R G P R G P P R G L H H Q R A Q L -
b  L L D G A R G G P P E A F T T S V R S Y -
c  C W T G P A G A P P R P S P P A C A A T -

CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGTGCTGCTGCG
421  -----+-----+-----+-----+-----+ 480
GGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCCGACCCCGACGACGACGC

a  P A Q H G D R R T A G E R G V G A A A A -
b  L P N T V T D A L R G S G A W G L L L R -
c  C P T R * P T H C G G A G R G G C C C A -

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FIG. 51

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a   P R G R R R A G S P A G T L R ? ? C A G -
b   R V G D D V L V H L L A R C A ? F V L V -
c   A W A T T C W F T C W H A A R ? L C W W -

GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCNAC
541 -----+-----+-----+-----+-----+ 600
CCNAGGGTCGACGCGGATGGTNCACACGCCCGGCGGACATGGTCGAGCCGCGACGNTG

a   G S Q L R L P ? V R A A A V P A R R C ? -
b   ? P S C A Y ? V C G P P L Y Q L G A A T -
c   ? P A A P T ? C A G R R C T S S A L ? L -

TCAGGCCCCGCCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCCT
601 -----+-----+-----+-----+-----+ 660
AGTCCGGGGCGGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA

a   S G P A P A T R ? W T R ? R L G S N G P -
b   Q A R P P P H A ? G P E ? V W D P T G L -
c   R P G P R H T L ? D P ? A S G I Q R A W -

GGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG
661 -----+-----+-----+-----+-----+ 720
CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCCGACGGTCGGGGCCACGCTCCTC

a   G T I A S G R P G S P W A A S P G C E E -
b   E P * R Q G G R G P P G L P A P G A R R -
c   N H S V R E A G V P L G C Q P R V R G G -

GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGGCGCTGC
721 -----+-----+-----+-----+-----+ 780
CGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGGGTTCTCCGGTCCGCACCGCGACG

a   A R G Q C Q P K S A V A Q E A Q A W R C -
b   R G G S A S R S L P L P K R P R R G A A -
c   A G A V P A E V C R C P R G P G V A L P -

CCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCACCCGGGCAGGACGCC
781 -----+-----+-----+-----+-----+ 840
GGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCGTCTCTGCGG

a   P * A G A D A R W A G V L G P P G Q D A -
b   P E P E R T P V G Q G S W A H P G R T P -
c   L S R S G R P L G R G P G P T R A G R L -

TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCCGCCGAAGAAGCCAC
841 -----+-----+-----+-----+-----+ 900
ACCTGGCTCACTGGCACCAAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG

a   W T E * P W F L C G V T C Q T R R R S H -
b   G P S D R G F C V V S P A R P A E E A T -
c   D R V T V V S V W C H L P D P P K K P P -

CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCGGCCAGCA
901 -----+-----+-----+-----+-----+ 960
GAGAAACCTCCACGCGAGAGACCGTGC GCGGTGAGGGTGGGTAGGCACCCGGCGGTCTGT

a   L F G G C A L W H A P L P P I R G P P A -
b   S L E G A L S G T R H S H P S V G R Q H -
c   L W R V R S L A R A T P T H P W A A S T -

CCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCTGGGACACGCTTGTCCCCCG
961 -----+-----+-----+-----+-----+ 1020
GGTGCGCCCGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC

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FIG. 51
(CONTINUED)

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a   P R G P P I H I A A T T S W D T P C P P -
b   H A G P P S T S R P P R P G T R L V P R -
c   T R A P H P H R G H H V L G H A L S P G -

GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
1021 -----+-----+-----+-----+-----+ 1080
CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCTGTGACGCNCGGAG

a   V Y A E T K H F L Y S S G D K ? T A ? L -
b   C T P R P S T S S T P Q A T ? T L R P S -
c   V R R D Q A L P L L L R R Q ? H C ? P P -

CTTCCTACTCAATATATCTGAGGCCAGCCTGACTGGCGTTTCGGGAGGTTTCGTGGAGACA
1081 -----+-----+-----+-----+-----+ 1140
GAAGGATGAGTTATATAGACTCCGGGTGCGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a   L P T Q Y I * G P A * L A F G R F V E T -
b   F L L N I S E A Q P D W R S G G S W R ? -
c   S Y S I Y L R P S L T G V R E V R G D ? -

NTCTTTCTGGTTCAGGCCTTGGATGCCAGGATTCCCCGAGGTTGCCCCGCCTGCCCCA
1141 -----+-----+-----+-----+-----+ 1200
NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACGGGGCGGACGGGGT

a   ? F L V P G L G C Q D S P Q V A P P A P -
b   S F W F Q A L D A R I P R R L P R L P Q -
c   L S G S R P W M P G F P A G C P A C P S -

GCGNTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCC
1201 -----+-----+-----+-----+-----+ 1260
CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCCTTGGTGCGCGTCACGGG

a   A ? L A N A A P V S G A A W E P R A V P -
b   R Y W Q M R P L F L E L L G N H A Q C P -
c   ? T G K C G P C F W S C L G T T R S A P -

CTACGGGGTGTTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGG
1261 -----+-----+-----+-----+-----+ 1320
GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTTCGGCC

a   L R G V P Q D A L P A A S C G H P S S R -
b   Y G V F L K T H C P L R A A V T P A A G -
c   T G C S S R R T A R C E L R S P Q Q P V -

TGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGAACACAG
1321 -----+-----+-----+-----+-----+ 1380
ACAGACACGGGCCCTCTTCGGGTCCCGAGACACCGCCGGGGCTCCTCCTCTGTGTGTC

a   C L C P G E A P G L C G G P R G G G T Q -
b   V C A R E K P Q G S V A A P E E E E H R -
c   S V P G R S P R A L W R P P R R R N T D -

ACCCCCGTGCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
1381 -----+-----+-----+-----+-----+ 1440
TGGGGGCAGCGGACCACGTTCGACGAGGCGGTTCGTGTCGTGCGGGACCGTCCACATGCCGA

a   T P V A W C S C S A S T A A P G R C T A -
b   P P S P G A A A P P A Q Q P L A G V R L -
c   P R R L V Q L L R Q H S S P W Q V Y G F -

TCGTGCGGGCCTGCCTGCGCCGGCTGGTGGCCCCAGGCCTCTGGGGCTCCAGGCACAACG
1441 -----+-----+-----+-----+-----+ 1500
AGCACGCCCGGACGGACGCGGCCGACCACGGGGTCCGGAGACCCCGAGGTCCGTGTGTC

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FIG. 51
(CONTINUED)

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a   S C G P A C A G W C P Q A S G A P G T T -
b   R A G L P A P A G A P R P L G L Q A Q R -
c   V R A C L R R L V P P G L W G S R H N E -

AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
1501 -----+-----+-----+-----+-----+ 1560
TTGCGGCGAAGGAGTTCCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA

a   N A A S S G T P R S S S P W G S M P S S -
b   T P L P Q E H Q E V H L P G E A C Q A L -
c   R R F L R N T K K F I S L G K H A K L S -

CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCC
1561 -----+-----+-----+-----+-----+ 1620
GCGACGTCTCTGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCAGCGCTCCTCGG

a   R C R S * R G R * A C G T A L G C A G A -
b   A A G A D V E D E R A G L R L A A Q E P -
c   L Q E L T W K M S V R D C A W L R R S P -

CAGGGGTGCGTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
1621 -----+-----+-----+-----+-----+ 1680
GTCCCAACCGACACAAGCGCGGCGTCTCGTGCGAGACGCACTCCTCTAGGACCGGTTCA

a   Q G L A V F R P Q S T V C V R R S W P S -
b   R G W L C S G R R A P S A * G D P G Q V -
c   G V G C V P A A E H R L R E E I L A K F -

TCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTATGTCA
1681 -----+-----+-----+-----+-----+ 1740
AGGACGTGACCGACTACTCACATGCAGCAGTTCGACGAGTCCAGAAAGAAAATACAGT

a   S C T G * * V C T S S S C S G L S F M S -
b   P A L A D E C V R R R A A Q V F L L C H -
c   L H W L M S V Y V V E L L R S F F Y V T -

CGGAGACCACGTTTCAAAGAAGCAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
1741 -----+-----+-----+-----+-----+ 1800
GCCTCTGGTGCAAAGTTTCTTGTCCGAGAAAAGATGGCCTTCTCACAGACCTCGTTCA

a   R R P R F K R T G S F S T G R V S G A S -
b   G D H V S K E Q A L F L P E E C L E Q V -
c   E T T F Q K N R L F F Y R K S V W S K L -

TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGCGAAG
1801 -----+-----+-----+-----+-----+ 1860
ACGTTTCGTAACCTTAGTCTGTGCTGAACCTTCTCCACGTGACGCCCTCGACAGCCTTC

a   C K A L E S D S T * R G C S C G S C R K -
b   A K H W N Q T A L E E G A A A G A V G S -
c   Q S I G I R Q H L K R V Q L R E L S E A -

CAGAGGTGAGGAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCA
1861 -----+-----+-----+-----+-----+ 1920
GTCTCCAGTCCGTGCTAGCCCTTCGGTCCGGCGGGACGACTGCAGGTCTGAGGCGAAGT

a   Q R S G S I G K P G P P C * R P D S A S -
b   R G Q A A S G S Q A R P A D V Q T P L H -
c   E V R Q H R E A R P A L L T S R L R F I -

TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGCGGAGCCAGAA
1921 -----+-----+-----+-----+-----+ 1980
AGGGGTTTCGACTGCCCCGACGCCGCTAACACTGTACCTGATGCAGCACCCCTCGGTCTT

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FIG. 51
(CONTINUED)

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a   S P S L T G C G R L * T W T T S W E P E -
b   P Q A * R A A A D C E H G L R R G S Q N -
c   P K P D G L R P I V N M D Y V V G A R T -

CGTTCGCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTACGCG
1981 -----+-----+-----+-----+-----+ 2040
GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC

a   R S A E K R G P S V S P R G * R H C S A -
b   V P Q R K E G R A S H L E G E G T V Q R -
c   F R R E K R A E R L T S R V K A L F S V -

TGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCTGGGCGCTGG
2041 -----+-----+-----+-----+-----+ 2100
ACGAGTTGATGCTCGCCCGCGCGGGGCGGAGGACCCGCGGAGACACGACCCGCGACC

a   C S T T S G R G A P A S W A P L C W A W -
b   A Q L R A G A A P R P P G R L C A G P G -
c   L N Y E R A R R P G L L G A S V L G L D -

ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCGCG
2101 -----+-----+-----+-----+-----+ 2160
TGCTATAGGTGTCCCGGACCGCGTGAAGCACGACGACACGCGCGGGTCTGGGCGGCG

a   T I S T G P G A P S C C V C G P R T R R -
b   R Y P Q G L A H L R A A C A G P G P A A -
c   D I H R A W R T F V L R V R A Q D P P P -

CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCAGGACA
2161 -----+-----+-----+-----+-----+ 2220
GACTCGACATGAAACAGTTCACCTACACTGCCCGCGCATGCTGTGGTAGGGGTCTGTGT

a   L S C T L S R W M * R A R T T P S P R T -
b   * A V L C Q G G C D G R V R H H P P G Q -
c   E L Y F V K V D V T G A Y D T I P Q D R -

GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGCGT
2221 -----+-----+-----+-----+-----+ 2280
CCGAGTGCCTCCAGTAGCGGTGCTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA

a   G S R R S S P A S S N P R T R T A C V G -
b   A H G G H R Q H H Q T P E H V L R A S V -
c   L T E V I A S I I K P Q N T Y C V R R Y -

ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
2281 -----+-----+-----+-----+-----+ 2340
TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA

a   M P W S R R P P M G T S A R P S R A T S -
b   C R G P E G R P W A R P Q G L Q E P R L -
c   A V V Q K A A H G H V R K A F K S H V S -

CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
2341 -----+-----+-----+-----+-----+ 2400
GATGGAAGTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCTNTTGT

a   L P * Q T S S R T C D S S W L T C R ? T -
b   Y L D R P P A V H A T V R G S P A G ? Q -
c   T L T D L Q P Y M R Q F V A H L Q ? N S -

GCCCCGTGAGGGATGCCGTCGTTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
2401 -----+-----+-----+-----+-----+ 2460
CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGACTTACTCCGGTCTGTAC

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FIG. 51
(CONTINUED)

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a   A R * G M P S S S S R A P P * M R P A V -
b   P A E G C R R H R A E L L P E * G Q Q W -
c   P L R D A V V I E Q S S S L N E A S S G -

GCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT
2461 -----+-----+-----+-----+-----+-----+ 2520
CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCTAGTCCCCGTTCA

a   A S S T S S Y A S C A T T P C A S G A S -
b   P L R R L P T L H V P P R R A H Q G Q V -
c   L F D V F L R F M C H H A V R I R G K S -

CCTACGTCCAGTGCCAGGGGATCCCCGAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
2521 -----+-----+-----+-----+-----+-----+ 2580
GGATGCAGGTACCGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG

a   P T S S A R G S R R A P S S P R C S A A -
b   L R P V P G D P A G L H P L H A A L Q P -
c   Y V Q C Q G I P Q G S I L S T L L C S L -

TGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTGCGCGGGACGGGCTGCTCC
2581 -----+-----+-----+-----+-----+-----+ 2640
ACACGATGCCGCTGTACCTTGTTCGACAAACGCCCTAAGCCGCCCTGCCCGACGAGG

a   C A T A T W R T S C L R G F G G T G C S -
b   V L R R H G E Q A V C G D S A G R A A P -
c   C Y G D M E N K L F A G I R R D G L L L -

TGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC
2641 -----+-----+-----+-----+-----+-----+ 2700
ACGCAAACACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGAAGG

a   C V W W M I S C W * H L T S P T R K P S -
b   A F G G * F L V G D T S P H P R E N L P -
c   R L V D D F L L V T P H L T H A K T F L -

TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTGCGGAAGACAG
2701 -----+-----+-----+-----+-----+-----+ 2760
AGTCTCTGGGACCAGGCTCCACAGGGACTCATACCGACGCCACTTGAACGCCTTCTGTC

a   S G P W S E V S L S M A A W * T C G R Q -
b   Q D P G P R C P * V W L R G E L A E D S -
c   R T L V R G V P E Y G C V V N L R K T V -

TGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
2761 -----+-----+-----+-----+-----+-----+ 2820
ACCACITGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC

a   W * T S L * K T R P W V A R L L F R C R -
b   G E L P C R R R G P G W H G F C S D A G -
c   V N F P V E D E A L G G T A F V Q M P A -

CCCACGGCCTATTCCCCTGGTGCGGCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA
2821 -----+-----+-----+-----+-----+-----+ 2880
GGGTGCCGATAAGGGGACCACGCCGACGACGACCTATGGGCCTGGGACCTCCACGTCT

a   P T A Y S P G A A C C W I P G P W R C R -
b   P R P I P L V R P A A G Y P D P G G A E -
c   H G L F P W C G L L L D T R T L E V Q S -

GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
2881 -----+-----+-----+-----+-----+-----+ 2940
CGCTGATGAGGTCGATACGGGCCTGGAGGTAGTCTCGGTGAGTGAAGTTGGCGCCGA

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FIG. 51
(CONTINUED)

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a   A T T P A M P G P P S E P V S P S T A A -
b   R L L Q L C P D L H Q S Q S H L Q P R L -
c   D Y S S Y A R T S I R A S L T F N R G F -

TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTACACA
2941 -----+-----+-----+-----+ 3000
AGTTCGACCCCTCCTTGTACGCAGCGTTTGAGAAACCCAGAACGCCGACTTCACAGTGT

a   S R L G G T C V A N S L G S C G * S V T -
b   Q G W E E H A S Q T L W G L A A E V S Q -
c   K A G R N M R R K L F G V L R L K C H S -

GCCTGTTTCTGGATTTCAGGTGAACAGCCCTCCAGACGGTGTGCACCAACATCTACAAGA
3001 -----+-----+-----+-----+ 3060
CGGACAAAGACCTAAACGTCCACTTGTGCGAGGTCTGCCACACGTGGTTGTAGATGTTCT

a   A C F W I C R * T A S R R C A P T S T R -
b   P V S G F A G E Q P P D G V H Q H L Q D -
c   L F L D L Q V N S L Q T V C T N I Y K I -

TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
3061 -----+-----+-----+-----+ 3120
AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTGAGGGTAAAGTAGTCG

a   S S C C R R T G F T H V C C S S H F I S -
b   P P A A G V Q V S R M C A A A P I S S A -
c   L L L Q A Y R F H A C V L Q L P F H Q Q -

AAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
3121 -----+-----+-----+-----+ 3180
TTCAAACCTTCTTGGGGGTGAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA

a   K F G R T P H F S C A S S L T R P P S A -
b   S L E E P H I F P A R H L * H G L P L L -
c   V W K N P T F F L R V I S D T A S L C Y -

ACTCCATCCTGAAAGCCAAGAACGCGAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGGCC
3181 -----+-----+-----+-----+ 3240
TGAGGTAGGACTTTCGGTCTTGTGCGTCCCTACAGCGACCCCGGTTCCCGCGGCGGCCGG

a   T P S * K P R T Q G C R W G P R A P P A -
b   L H P E S Q E R R D V A G G Q G R R R P -
c   S I L K A K N A G M S L G A K G A A G P -

CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTC
3241 -----+-----+-----+-----+ 3300
GAGACGGGAGGCTCCGGCACGTACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG

a   L C P P R P C S G C A T K H S C S S * L -
b   S A L R G R A V A V P P S I P A Q A D S -
c   L P S E A V Q W L C H Q A F L L K L T R -

GACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCAGCTGA
3301 -----+-----+-----+-----+ 3360
CTGTGGCACAGTGGATGCACGGTGAGGACCCAGTGAGTCCTGTGCGGTCTGCGTCACT

a   D T V S P T C H S W G H S G Q P R R S * -
b   T P C H L R A T P G V T Q D S P D A A E -
c   H R V T Y V P L L G S L R T A Q T Q L S -

GTCGGAAGCTCCCGGGGACGACGTGACTGCCCTGGAGGCCGAGCCAACCCGGCACTGC
3361 -----+-----+-----+-----+ 3420
CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGGCGTCCGTTGGGCGGTGACG

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FIG. 51
(CONTINUED)

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a      V G S S R G R R * L P W R P Q P T R H C -
b      S E A P G D D A D C P G G R S Q P G T A -
c      R K L P G T T L T A L E A A A N P A L P -

CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCA
3421 -----+-----+-----+-----+-----+ 3480
GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCTGGTCCGGCTCTCGT

a      P Q T S R P S W T D G H P P T A R P R A -
b      L R L Q D H P G L M A T R P Q P G R E Q -
c      S D F K T I L D * W P P A H S Q A E S R -

GACACCAGCAGCCCTGTCAAGCCGGCTCTACGTCCCAGGGAGGGGGCGGCCACAC
3481 -----+-----+-----+-----+-----+ 3540
CTGTGGTGTCTGGGACAGTGCAGCCCGAGATGCAGGGTCCCTCCCTCCCGCCGGGTGTG

a      D T S S P V T P G S T S Q G G R G G P H -
b      T P A A L S R R A L R P R E G G A A H T -
c      H Q Q P C H A G L Y V P G R E G R P T P -

CCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTGCATGT
3541 -----+-----+-----+-----+-----+ 3600
GGTCCGGGCGTGGCGACCTCAGACTCCGGACTCACTCACAACCGGCTCCGGACGTACA

a      P G P H R W E S E A * V S V W P R P A C -
b      Q A R T A G S L R P E * V F G R G L H V -
c      R P A P L G V * G L S E C L A E A C M S -

CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
3601 -----+-----+-----+-----+-----+ 3660
GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCTGGTTCCCGACTCAC

a      P A E G * V S G * G L S E C P A K G * V -
b      R L K A E C P A E A * A S V Q P R A E C -
c      G * R L S V R L R P E R V S S Q G L S V -

TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCAGGGCC
3661 -----+-----+-----+-----+-----+ 3720
AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG

a      S S T P A V F T S P Q A G A R L H P R A -
b      P A H L P S S L P H R L A L G S T P G P -
c      Q H T C R L H F P T G W R S A P P Q G Q -

AGCTTTTCCTCACCAGGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
3721 -----+-----+-----+-----+-----+ 3780
TCGAAAAGGAGTGGTCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT

a      S F S S P G A R L P L P T * E * S I P R -
b      A F P H Q E P G F H S P H R N S P S P D -
c      L F L T R S P A S T P H I G I V H P Q I -

TTGCCCATTTGTTACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTG
3781 -----+-----+-----+-----+-----+ 3840
AAGCGGTAACAAGTGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC

a      F A I V H P S P C P P L P S T P T I Q V -
b      S P L F T P R P A L L C L P P P P S R W -
c      R H C S P L A L P S F A F H P H H P G G -

GAGACCCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
3841 -----+-----+-----+-----+-----+ 3900
CTCTGGGACTCTTCTGGGACCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC

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FIG. 51
(CONTINUED)

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a E T L R R T L G A L G I W S D Q R C A L -
 b R P * E G P W E L W E F G V T K G V P C -
 c D P E K D P G S S G N L E * P K V C P V -

 TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
 3901 -----+-----+-----+-----+-----+ 3960
 ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCTCCA

 a Y T G E D P A P G W G S L W V K L G G G -
 b T Q A R T L H L D G G P C G S N W G E V -
 c H R R G P C T W M G V P V G Q I G G R C -

 GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
 3961 -----+-----+-----+-----+-----+ 4020
 CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAACTTTTTTTTTTTTTTTT

 a A V G V K Y * I Y E F F S F E K K K K K -
 b L W E * N T E Y M S F S V L K K K K K K -
 c C G S K I L N I * V F Q F * K K K K K K -

 AAAAAAAAAA
 4021 ----- 4029
 TTTTTTTT

 a K K K -
 b K K -
 c K K -

FIG. 51
(CONTINUED)

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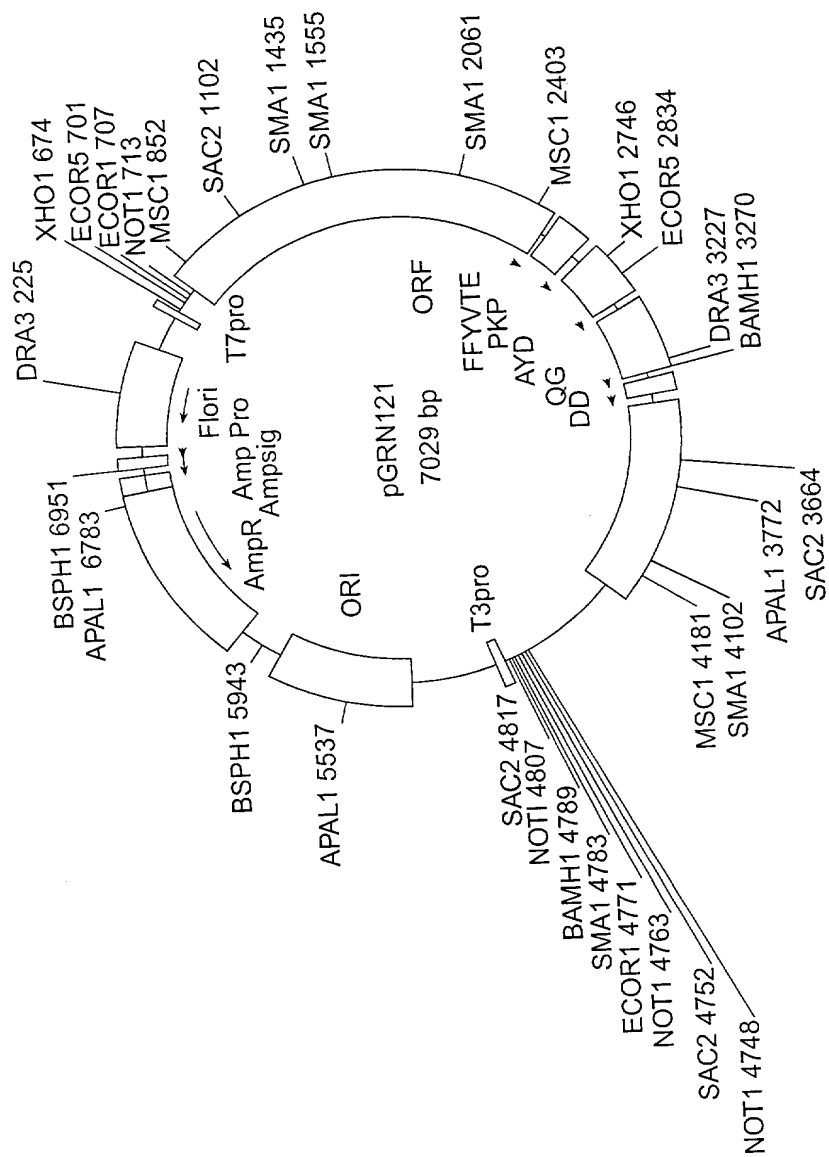


FIG. 52

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1
 met
 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG
 10
 pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC
 20
 his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG
 30
 gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT
 40
 phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC
 50
 ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC
 60
 leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC
 70
 gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG
 80
 ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
 90
 tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
 TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG
 100
 trp gly leu leu leu arg arg val gly asp asp val leu val his
 TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC
 110
 leu leu ala arg cys ala leu phe val leu val ala pro ser cys
 CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC
 120
 ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
 GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC
 130
 thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
 ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

FIG. 53

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200 leu gly cys glu arg ala trp asn his ser val arg glu ala gly
 CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG
 210
 220 val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
 GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC
 230 ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
 AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC
 240
 250 ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
 GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG
 260 ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
 GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT
 270
 280 val val ser pro ala arg pro ala glu glu ala thr ser leu glu
 GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
 290 gly ala leu ser gly thr arg his ser his pro ser val gly arg
 GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC
 300
 310 gln his his ala gly pro pro ser thr ser arg pro pro arg pro
 CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC
 320 trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
 TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC
 330
 340 leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
 CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA
 350 leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
 CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG
 360
 370 glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
 GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC
 380 arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
 CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC
 390
 400 leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
 CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG
 410 val leu leu lys thr his cys pro leu arg ala ala val thr pro
 GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA
 420

FIG. 53
(CONTINUED)

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430
 ala ala gly val cys ala arg glu lys pro gln gly ser val ala
 GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440 450
 ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
 GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
 leu arg gln his ser ser pro trp gln val tyr gly phe val arg
 CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
 ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
 GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
 his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
 leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
 CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
 met ser val arg asp cys ala trp leu arg arg ser pro gly val
 ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
 gly cys val pro ala ala glu his arg leu arg glu glu ile leu
 GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
 ala lys phe leu his trp leu met ser val tyr val val glu leu
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
 arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

FIG. 53
(CONTINUED)

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650 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760 his gly his val arg lys ala phe lys ser his val ser thr leu
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

770 thr asp leu gln pro tyr met arg gln phe val ala his leu gln
 ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

790 glu thr ser pro leu arg asp ala val val ile glu gln ser ser
 GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

800 ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
 TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

820 phe met cys his his ala val arg ile arg gly lys ser tyr val
 TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

830 gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
 CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

850 cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
 TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

860 ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
 ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

870

FIG. 53
(CONTINUED)

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880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

900
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

910
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

920
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

930
ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

940
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

950
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

960
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

970
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

980
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

990
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1000
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1010
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1020
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIG. 53
(CONTINUED)

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1100 1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC
AGGCCCCGACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTGCATGTCC
GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCC
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
CGCCATTGTTACCCYTCGCCCTGCCYTCTTTGCCTTCCACCCCCACCATCCAGGTGGA
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAA
AAAAAAAAA

FIG. 53
(CONTINUED)

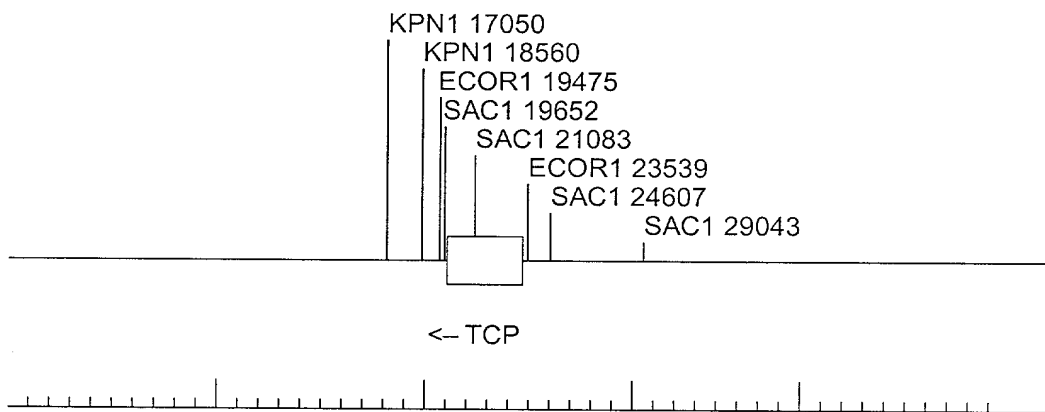


FIG. 54